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TITLE: Identification of Biomarkers Associated with the Healing
of Chronic Wounds

PRINCIPAL INVESTIGATOR: Laura E. Edsberg, Ph.D.

CONTRACTING ORGANIZATION: Daemen College
Amherst, NY 14226

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Laura E. Edsberg, Ph.D.

email: Ledsberg@daemen.edu

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The fact that there are differences in chronic versus normal healing wounds is well documented. What is unknown at this time are the specific biomarkers associated with normal healing wounds. The initial objective of this study was to identify the biomarkers associated with the earliest stages of healing in chronic wounds. The objectives of the continuation of the initial project were to evaluate the biochemical profiles of healing burns and compare those with hypertrophic scarring with those without. The findings of this study are intended to facilitate the development a diagnostic tool, which would assist in the evaluation of the healing process in chronic and burn wounds.

15. SUBJECT TERMS

Chronic wound, burn wounds, healing, hypertrophic scarring, 2D Page, iTRAQ, antibody arrays, PIXIES

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1. INTRODUCTION: Narrative that briefly (one paragraph) describes the subject, purpose and scope of the research.

The 10 year period of this work begins with the project focused on pressure ulcers and then the continuation project focused on hypertrophic scarring in burn wounds. There are 2 distinct SOW for the 2 area of research. Each SOW is listed below and the description of the completion of the SOW is described.

The fact that there are differences in chronic versus normal healing wounds is well documented. What is unknown at this time are the specific biomarkers associated with healing wounds, the role each of these biomarkers play in wound healing, and the biomarkers that can serve as the earliest predictors of healing. It is our hypothesis that specific cytokines, proteases, and growth factors serve as the earliest indicators of healing in chronic wounds. The initial objective of this study was to identify the biomarkers associated with the earliest stages of healing in chronic wounds. Hypertrophic scarring is a common complication associated with healed deep burns. It is our hypothesis that specific quantifiable biochemical differences in the sera and burn fluid exist between burn patients that develop hypertrophic scarring and those that do not. The objectives of the continuation of the initial project were to evaluate the biochemical profiles of healing burns and compare those with hypertrophic scarring with those without. The findings of this study are intended to facilitate the development a diagnostic tool, which would assist in the evaluation of the healing process in chronic and burn wounds.

2. KEYWORDS: Provide a brief list of keywords (limit to 20 words).
Chronic wound, burn wounds, healing, hypertrophic scarring, 2D Page, iTRAQ, antibody arrays, PIXIES

3. OVERALL PROJECT SUMMARY:
Statement of Work (Pressure Ulcer)

Technical Objective 1: To identify the biochemical changes that occur as a chronic wound begins the healing process.

- a. Analyze fluid samples to determine proteins present
- b. Identify differences between subjects and subject time points
- c. Confirm protein identities

Technical Objective 2: To assess the rate of healing of the wounds analyzed.

- a. Measure wound
- b. Calculate trajectories of healing for wounds over time

Technical Objective 3: To evaluate the location of the biomarkers assessed.

- a. Compare proteins found in different locations using protein analysis

Technical Objective 4: To identify the earliest changing biomarkers occurring in wounds which progressed toward healing.

- a. Correlate the changes in wound chemistry with the rate of healing
- b. Analyze the earliest biochemical changes present

STATEMENT OF WORK (Burn)

Continuation

Burn Fluid and Patient Sera Biochemical Analysis as an Indicator of Aberrant Wound Repair and Hypertrophic Scarring

Phase I:

Technical Objective 1: Characterize the protein biochemistry of burn wounds.

- a. Analyze wound fluid samples to determine proteins present
- b. Identify trends present in burns as healing occurs

Technical Objective 2: Characterize the protein biochemistry in the sera of subjects with burn wounds.

- a. Analyze sera to determine the proteins present
- b. Identify trends present in subjects with burns during healing

Technical Objective 3: Assess the presence of hypertrophic scarring.

- a. Burn Scar Index (Vancouver Scar Scale) parameters of scar will be assessed
- b. Identify subjects with hypertrophic scarring burn wounds

Technical Objective 4: Correlate the differences between the sera and burn fluid samples during healing and identify biochemical differences between hypertrophic scarring and non-hypertrophic scarring subjects.

- a. Correlate the trends in wound and sera biochemistry during healing
- b. Correlate clinical outcome with biochemistry
- c. Identify the differences present in sera and wound exudates in samples from subjects with hypertrophic scarring

Phase II:

Technical Objective 1: Develop a porcine model for burn wounds (second degree - superficial and deep).

- a. Develop methods to reproducibly induce cutaneous thermal injuries in porcine tissue model.
- b. Collect wound fluid from thermally injured swine for proteins of clinical interest, based upon those identified in Phase I of this project.

Technical Objective 2: Characterize the protein biochemistry of porcine wound fluids.

- a. Analyze burn wound fluid by both ELISA and PIXIES.
- b. Compare results from PIXIES with those from ELISA.

Technical Objective 3: Evaluate and validate porcine data with those obtained from Phase I studies.

- a. Compare wound fluid biochemistry from thermally injured swine to that from normally-healing human wound fluid from Phase I of the study.

Pressure Ulcer

Technical Objective 1: To identify the biochemical changes that occur as a chronic wound begins the healing process.

- c. Analyze fluid samples to determine proteins present
- d. Identify differences between subjects and subject time points
- c. Confirm protein identities

Using two-dimensional polyacrylamide gel electrophoresis (2D Page) it was found that healed wounds showed an increased number of spots coincident with wound closure, while unhealed wounds showed no temporal trend (Wyffels JT, Fries KM, Randall J, Ha D, Lodwig C, Brogan M, Shero M, Edsberg LE. Analysis of chronic pressure ulcer wound fluid using two-dimensional electrophoresis. *International Wound Journal* 2010;7:236-248.). Ultimately 2D-gel proved to be a less than ideal method to search for biomarkers in chronic wound fluid. Though this 2D proteomic approach has proven successful for biomarker discovery in other systems, because of the high numbers of spots present in gels, as well as the complexity of spots, high cost of protein identification from gel plugs and sample consumption, further biomarker identification via 2D technology was abandoned in favor other techniques including iTRAQ and label-based microarrays that simultaneously measure a panel of proteins for a more complete assessment of the proteome.

The final methodology developed to screen the wound fluid samples for potential targets and analyze and quantify the proteins of interest consists of antibody arrays and multiplexed isobaric tagging technology (iTRAQ™). iTRAQ identifies the most abundant proteins present and the least abundant include most cytokines, which is the majority of what has been previously reported in the literature regarding the biochemistry of pressure ulcers and other types of wounds. As a result, the inclusion of antibody arrays allows samples to be analyzed for the less abundant and smaller proteins.

The relative change in protein amount as compared to other samples/days was been analyzed for the samples and significant differences in the proteins present in healed versus chronic wounds and interior versus peripheral locations in the wound were identified. The following proteins had no significant increases or decreases between groups or over time: Actin, alpha cardiac muscle 1, angiotensinogen precursor, Ig kappa chain V-I region Kue, peptidoglycan, periostin precursor (PN), rab GDP dissociation inhibitor beta, and ras-related C3 botulinum toxin substrate 1 precursor. The following proteins were present in healed wounds only: Calreticulin precursor, Carcinoembryonic antigen-related cell adhesion molecule 8 precursor, Cytidine deaminase, Elongation factor 1-delta, Elongation factor 1-gamma, Hypoxanthine-guanine, Keratin type II (CK-5), Peroxiredoxin-2, and Protein DJ-1. The above proteins were never found in chronic

wound samples. The proteins found only in chronic wounds and never in healed to date include: Netrophil gelatinase-associated lipocalin precursor (NGAL), Protein S100-A9, Actin, Calmodulin-like protein 3, Hemoglobin subunit beta, and Vitronectin precursor (s-protein) (Edsberg, LE, Wyffels JT, Brogan MS, Fries KM. Analysis of the Proteomic Profile of Chronic Pressure Ulcers. Wound Repair Regeneration 2012;20:378-401).

The iTRAQ data were analyzed using Ingenuity Pathway Analysis Software (IPA), a software package that allows analysis, modeling, and literature searches for similar proteins. The molecular and cellular function identified to have the largest number of molecules present in the samples was cellular movement. This was the case in both healed and chronic wounds in both internal and peripheral locations. In a wound, cellular movement is necessary for healing to occur. Cell death had a large number of molecules present in chronic wounds in both the internal and peripheral locations. These molecules were not present in internal sites of healed wounds, but were present in some peripheral locations of healed wounds. This may be significant in the identification of differences in both location, as well as clinical outcome of wounds. Antigen presentation had many molecules present in IPA analysis in both the internal and peripheral locations of chronic wounds.

Analysis of regulated molecules found in the iTRAQ experiments revealed that ENO1 was down regulated in healed wounds in both internal and peripheral locations and upregulated in chronic wounds in both internal and peripheral locations. ENO1 works to create and activate collagenase and degrades fibrin and extracellular matrix. The upregulation in chronic wounds is consistent with the role of ENO1. Also, S100A8 and S100A9 were upregulated in internal sites of chronic wounds only. These inflammatory markers and others within the S100 family are of great interest as potential markers of chronic wounds.

Technical Objective 2:

To assess the rate of healing, the wounds were photographed and their area calculated at each time point. All wounds were separated by clinical outcome into healed, healing, and chronic categories based on area measurements over the 42 days. The manuscript based on the models tested for wound measurement and clinical outcome prediction was published in Ostomy Wound

Management (Edsberg LE, Wyffels JT, Ha D. Longitudinal study of stage III and stage IV pressure ulcer area and perimeter as healing parameters to predict wound closure. *Ostomy Wound Management* 2011;57(10):50-62). No correlation between tissue type present and wound outcome was found. The presence of granulation tissue is a positive clinical sign in the clinical assessment of a chronic wound bed, but the presence of granulation tissue did not correlate with healing in chronic pressure ulcers (Wyffels JT, Edsberg LE. Granulation tissue of chronic pressure ulcers as predictive indicator of wound closure. *Advances in Skin & Wound Care* 2011;24(10):464-473). The tissue type and clinical outcome correlation was examined as part of the search for potential biomarkers of healing. While these changes may occur, their lack of correlation with outcome makes these biochemical changes a poor choice for potential biomarkers.

Technical Objective 3:

To evaluate the location of the biomarkers assessed, samples were collected from both the peripheral and interior locations on each wound at each time point. Samples from interior location of the wound had higher protein concentrations than samples collected from the wound periphery for all outcomes ($p=0.000$). Ulcer stage and protein concentration were correlated with high protein concentrations resulting from deeper ulcers ($p=0.000$). Samples contaminated with blood had higher protein concentrations than those free of blood for both internal and peripheral swab samples from all outcomes ($p=0.000$). This result was confirmed using a Student's t-test with matched samples where both bloody and non-bloody swabs were collected for the same wound on the same day.

Day did not have a significant effect on protein concentration when all outcomes were combined. Additional analyses of each outcome independently had similar results with significance associated with unhealed/chronic ulcers only. The ability of total protein concentration to be used as an indicator of wound status or outcome was further tested using a differential function analysis but no significant models resulted. There was not a statistically significant correlation between wound fluid total protein concentration and clinical outcome.

Interior and periphery swabs matched by day for four chronic wounds on seven days were used to compare cytokine concentration between sampling locations. Proteins with more than one significant iTRAQ ratio ($p < 0.1$) and matching directionality among days were selected. Four proteins, pyruvate kinase isozymes M1/M2 (PKM2), profilin-1 (PFN1), Ig lambda-1 chain C regions (IGLC1) and Ig gamma-1 chain C region (IGHG1) were present in lower levels for periphery samples when compared to interior samples and six proteins, keratin, type II cytoskeletal 6A (KRT6A), keratin, type I cytoskeletal 14 (KRT14), S100A7, Alpha-1-antitrypsin precursor (SERPINA1), hemoglobin subunit alpha (HBA1) and hemoglobin subunit beta (HBB), were present in higher levels in periphery samples when compared to interior samples. To identify protein level trends during the healing process, the iTRAQ ratios of adjacent time points were compared among healed wounds. No consistent trends were identified in either interior or periphery samples.

Due to the lack of periphery samples in healed wounds, only chronic wounds were used to compare protein levels between interior and periphery samples Using Wilcoxon Signed Ranks Test, seven proteins with lower concentrations in periphery samples when compared to interior samples, and three proteins with higher protein levels in periphery samples when compared to interior samples were identified. These included S100A7, which was also identified in iTRAQ data.

Technical Objective 4:

The wound fluid from 32 subjects with 42 pressure ulcers was evaluated over 6 weeks at 15 time points. Samples specific to both the interior and the periphery of the wound bed were collected. Antibody screening arrays, isobaric tags for relative and absolute quantitation with mass spectrometry and multiplexed microarrays were used to characterize wound fluid and results were correlated with clinical outcome. Twenty-one proteins were found to distinguish between healed and chronic wounds and 19 proteins were differentially expressed between the interior and periphery of wounds. Four proteins, pyruvate kinase isozymes M1/M2, profilin-1, Ig lambda-1 chain C regions, and Ig gamma-1 chain C region, were present in lower levels for periphery samples when compared to interior samples and six proteins, keratin, type II

cytoskeletal 6A (KRT6A), keratin, type I cytoskeletal 14, S100 calcium binding proteins A7, alpha-1-antitrypsin precursor, hemoglobin subunit alpha, and hemoglobin subunit beta, were present in higher levels in periphery samples when compared with interior samples. S100 calcium binding protein A6, S100 calcium binding protein A7, and soluble receptor for advanced glycation end-products had higher levels in the periphery of chronic wounds vs. the interior in planar arrays. A mixed linear model was built for each protein to compare temporal trends in concentration between healed and chronic samples. Among 58 proteins, only one protein had significant values for all four parameters in the model, MIG, synonymous with chemokine (C-X-C motif) ligand 9 (CXCL9). CXCL9 increased as wounds healed and remained nearly constant or decreased slightly for ulcers that were not approaching closure. The lack of significance for other cytokines using the linear mixed model, as well as other nonlinear models, can likely be attributed in part to the high individual variation of protein levels compared with the small number of observations and the small between-group variation (Edsberg, LE, Wyffels JT, Brogan MS, Fries KM. Analysis of the Proteomic Profile of Chronic Pressure Ulcers. Wound Repair Regeneration 2012;20:378-401).

Continuation to Project

Burn Fluid and Patient Sera Biochemical Analysis as an Indicator of Aberrant Wound Repair and Hypertrophic Scarring

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Phase I:

Technical Objective 1: Characterize the protein biochemistry of burn wounds.

- a. Analyze wound fluid samples to determine proteins present
- e. Identify trends present in burns as healing occurs

The initial hurdle with this objective was enrollment and collection of wound fluid appropriate for analysis. Initially we sought to swab wounds, but not enough protein was present in the wound bed at times. Ultimately we chose to collect dressings and extract wound fluid

from the dressings and collect swabs. Swabs were preferred, but if not enough protein was present we used fluid collected from dressings.

Survey Arrays

The analysis of the wound fluid began with a broad survey tool Kinex™ Antibody Microarray (KAM) a single dye, non-competitive sample binding methodology. The survey included 510 pan-specific antibodies that measure 189 unique protein kinases, 31 protein phosphatases and 142 regulatory subunits of these enzymes and other cell signaling proteins that regulate cell proliferation, stress, and apoptosis and approximately 340 phosphosite-specific antibodies that track the non-redundant phosphorylation of 128 sites in protein kinases, 4 sites in protein phosphatases, and 155 sites in other cell signaling proteins. Lysate protein from each sample was covalently labeled with a fluorescent dye combination. Free dye molecules were then removed at the completion of labeling reactions by gel filtration. After blocking non-specific binding sites on the array, an incubation chamber was mounted onto the microarray to permit the loading of 2 samples side by side on the same chip and prevent mixing of the samples. Following sample incubation, unbound proteins are washed away. Each array produces a pair of 16-bit images, which are captured with a Perkin-Elmer ScanArray Reader laser array scanner (Waltham, MA). Signal quantification is performed with ImaGene 9.0 from BioDiscovery (El Segundo, CA) with predetermined settings for spot segmentation and background correction. The background-corrected raw intensity data are logarithmically transformed with base 2. Since Z normalization in general displays greater stability as a result of examining where each signal falls in the overall distribution of values within a given sample, as opposed to adjusting all of the signals in a sample by a single common value, Z scores are calculated by subtracting the overall average intensity of all spots within a sample from the raw intensity for each spot, and dividing it by the standard deviations (SD) of all of the measured intensities within each sample. Z ratios are further calculated by taking the difference between the averages of the observed protein Z scores and dividing by the SD of all of the differences for that particular comparison. Calculated Z ratios have the advantage that they can be used in multiple comparisons without further reference to the individual conditional standard deviations by which they were derived. A Z ratio of ± 1.2 to ± 1.5 is inferred as significant. One problem with Z ratios is that they do not take into account the intensity of the signals, and closer replicates can make the Z ratios appear high even though the

magnitude of the change in averages may be relatively small. Therefore, the changes in spot intensity between control and treatment samples as the percent change from control (%CFC) using globally normalized data are also determined. Targets were defined as Priority lead based on selection criteria: %CFC ≥ 50 ; SUM of %Error Ranges $< 0.75 \times$ %CFC value; At least one Globally Normalized intensity value ≥ 1500 . Targets were defined as Possible lead selection based on criteria: %CFC ≥ 50 ; SUM of %Error Ranges $< 0.85 \times$ %CFC value; At least one Globally Normalized intensity value ≥ 1000

Wound fluid samples from individuals with hypertrophic scars (H+) and samples from individuals without hypertrophic scars (H-) were compared in 4 different arrays. The first array compared pooled H+ to pooled H- wound fluid samples. Two arrays were used to examine samples over time. The first time point array evaluated samples from a H+ subject 2 days apart and the second evaluated samples from a different H+ subject 4 days apart. An array comparing H+ and H- within the same subject compared wound fluid from a H+ burn injury and wound fluid from a H- donor graft site.

The targets identified in the pooled H+ vs. pooled H- array are shown in Table 1.

Target Protein Name	Phospho Site (Human)	Best Leads	Z-ratio (H+, H-)
Striatin	Pan-specific	Priority	3.17
GSK3a	Y284+Y285	Priority	2.28
PRKWNK4	Pan-specific	Priority	2.02
Fes	Pan-specific	Priority	1.84
MST3	T190	Priority	1.72
Crystallin aB	Pan-specific	Priority	1.63
Src	Pan-specific	Priority	1.67
Hsp27	S15	Priority	1.55
TYK2	Pan-specific	Priority	1.45
PACSIN1	Pan-specific	Priority	1.58
Catenin b	Pan-specific	Priority	1.64
SPHK1	Pan-specific	Priority	1.54
DUSP2	Pan-specific	Priority	1.37
DUSP11	Pan-specific	Priority	1.43
FAK	Pan-specific	Priority	1.57
Nek7	Pan-specific	Priority	1.46
VEGFR2	Y1059	Priority	1.50
CK2a	Pan-specific	Priority	1.40

ERK3	Pan-specific	Priority	1.43
PKCg	T514	Priority	1.49
LKB1	Pan-specific	Priority	1.29
Tyro10	Pan-specific	Priority	1.40
PYKSD8	pTyr	Priority	1.22
SHP2	Pan-specific	Priority	1.25
ERK5	T219+Y221	Priority	1.21
PCTK1	Pan-specific	Priority	1.33
SMC1	S957	Priority	1.25
Hsp25	Pan-specific	Priority	1.16
ERK1	Y204	Priority	1.23
COT	Pan-specific	Priority	1.17
ERK4	S186	Priority	1.12
PKCm (PKD)	S916	Priority	1.24
CaMK4	T200	Priority	1.08
Cyclin A	Pan-specific	Priority	1.07
BCKD (BCKDK)	Pan-specific	Priority	1.13
JNK 1/2/3	T183/Y185	Priority	1.13
PKCg	Pan-specific	Priority	1.22
MELK	Pan-specific	Priority	-1.98
JAK2	Pan-specific	Priority	-1.98
PAKg	Pan-specific	Priority	-1.94
Nlk	Pan-specific	Priority	-1.96
JAK2	Pan-specific	Priority	-2.25
Ikb Kinase alpha	Pan-specific	Priority	-2.16
STAT4	Pan-specific	Priority	-2.02
Akt1 (PKBa)	S473	Priority	-2.04
PKR1	Pan-specific	Priority	-2.11
Snk	Pan-specific	Priority	-2.35
Hpk1	Pan-specific	Priority	-2.55
NIK	Pan-specific	Priority	-2.65
GADD 153 (CHOP)	Pan-specific	Priority	-2.87
YSK1	Pan-specific	Priority	-3.35
PDK1	Pan-specific	Priority	-3.87
Mnk2	Pan-specific	Priority	-4.28
PKN	Pan-specific	Priority	-4.62
Progesterone Receptor	S294	Priority	-7.62
Estrongen Receptor	S104	Possible	1.96
VAV1	Y826	Possible	1.66
TYK2	Pan-specific	Possible	1.52
MAPKAPK5	T186	Possible	1.15
JAK3	Pan-specific	Possible	-2.17

Table 1. Pooled H+ vs. H- wound fluid target proteins identified.

Targets identified in the samples taken from an H+ burn injury at 2 time points 4 days apart are shown in Table 2.

Target Protein Name	Phospho Site (Human)	Best Leads	Z-ratio (9S1, 9)
JNK1	Pan-specific	Priority	2.58
FGFR2	Pan-specific	Priority	2.49
GADD 153 (CHOP)	Pan-specific	Priority	2.48
WNK3	Pan-specific	Priority	2.36
VGFR2	Pan-specific	Priority	2.32
WNK2	Pan-specific	Priority	2.26
PDGFRa	Pan-specific	Priority	2.27
MELK	Pan-specific	Priority	2.15
MEK5	Pan-specific	Priority	2.11
PP4/A'2	Pan-specific	Priority	2.04
Met	Pan-specific	Priority	2.02
PDGFRa	Pan-specific	Priority	2.01
EGFR	Pan-specific	Priority	1.95
EGFR	Pan-specific	Priority	1.92
PKCg	T655	Priority	1.84
AurKA	Pan-specific	Priority	1.78
JAK2	Pan-specific	Priority	1.69
Cdc25C	Pan-specific	Priority	1.69
Hsp27	S78	Priority	1.70
JNK 1/2/3	T183/Y185	Priority	1.66
Cdc25B	Pan-specific	Priority	1.62
eIF4G	S1108	Priority	1.69
MEK5	Pan-specific	Priority	1.68
Src	Pan-specific	Priority	1.67
Hsp70	Pan-specific	Priority	1.61
MEK2	Pan-specific	Priority	1.55
Flt3	Pan-specific	Priority	1.53
MKK3	S218	Priority	1.50
hsp90b	Pan-specific	Priority	1.51
AurKB	S227	Priority	1.48
FRK	Y387	Priority	1.50
GluR1	S849	Priority	1.55
DUSP9	Pan-specific	Priority	1.46
ZIPK	Pan-specific	Priority	1.50
STAT5A	Pan-specific	Priority	1.50
VGFR2	Pan-specific	Priority	1.44
STAT5	Y694	Priority	1.45
JAK3	Pan-specific	Priority	1.32
Cdc25A	Pan-specific	Priority	1.32
FGFR2	Pan-specific	Priority	1.22
CREB1	S133	Priority	1.27

PARP1	Pan-specific	Priority	1.20
AAK1	S637	Priority	1.25
EGFR	Y998	Priority	1.23
AurKA	Pan-specific	Priority	1.16
IGF1R	Y1280	Priority	1.26
CytoC	Pan-specific	Priority	1.23
ERK2	Pan-specific	Priority	1.13
EGFR	Pan-specific	Priority	1.09
PCTK1	Pan-specific	Priority	1.20
Hpk1	Pan-specific	Priority	1.17
MEKK-NT	Pan-specific	Priority	1.12
FGFR3	Pan-specific	Priority	1.12
PP2A B' (B56)	Pan-specific	Priority	1.08
ERK2	Pan-specific	Priority	1.10
Cyclin A	Pan-specific	Priority	1.07
Raf1	Pan-specific	Priority	1.11
JAK3	Pan-specific	Priority	1.01
MLK3	T277+S281	Priority	1.07
VIM	Y117	Priority	1.08
Crystallin aB	S19	Priority	1.09
Nek2	S171	Priority	0.98
MDM2	S166	Priority	1.07
Cdc25C	Pan-specific	Priority	1.02
ERK5	T219+Y221	Priority	1.01
ERK4	S186	Priority	1.00
CDK1/2	Y14/Y15	Priority	1.02
PP2A/Bg2	Pan-specific	Priority	0.98
eIF4E	S209	Priority	1.01
CAMK2d	Pan-specific	Priority	0.97
ERK5	Y221	Priority	0.89
TYK2	Pan-specific	Priority	0.92
MKK7	Pan-specific	Priority	0.91
Hsp40	Pan-specific	Priority	0.89
Met	T1241	Priority	0.89
SPHK2	Pan-specific	Priority	0.87
MEK4	S257/T261	Priority	0.90
Kit	Pan-specific	Priority	0.79
Hsp90	Pan-specific	Priority	0.89
CSF1R	Pan-specific	Priority	0.86
Ret	Pan-specific	Priority	0.85
ErbB2	Pan-specific	Priority	0.81
ErbB4	Pan-specific	Priority	0.81
SOCS4	Pan-specific	Priority	0.83
TYK2	Pan-specific	Priority	0.85
CaMK2a	T286	Priority	0.76
Cyclin G1	Pan-specific	Priority	0.84
CaMKK	Pan-specific	Priority	0.81

MKK4	Pan-specific	Priority	0.72
PPP1R11	Y64	Priority	0.79
VEGF-C	Pan-specific	Priority	0.81
PDK1	Pan-specific	Priority	0.72
IGF1R	Y1346	Priority	0.78
JNK3	Pan-specific	Priority	0.73
ErbB2	T686	Priority	0.70
TrkB	Pan-specific	Priority	0.75
DGKZ	Pan-specific	Priority	0.72
ErbB2	Y1248	Priority	0.68
COT	Pan-specific	Priority	0.70
ErbB4	Pan-specific	Priority	-1.94
A-Raf	Pan-specific	Priority	-1.92
B-Raf	S446+S447	Priority	-1.97
BRCA1	S1497	Priority	-1.88
CDK4	T172	Priority	-2.14
Ros	Pan-specific	Priority	-2.87
FRS2	Y349	Possible	2.84
STAT3	Y704	Possible	2.58
STAT1	Pan-specific	Possible	2.41
CDK2	Pan-specific	Possible	1.80
Abl	Pan-specific	Possible	1.71
GCK	Pan-specific	Possible	1.10
PKCd	Y311	Possible	1.10
EGFR	Y1148	Possible	1.12
PAKg	Pan-specific	Possible	1.01
Bak	Pan-specific	Possible	0.98
NFkappaB p65	Pan-specific	Possible	0.88
Tyro10	Pan-specific	Possible	0.80
PKCa	Pan-specific	Possible	-1.62

Table 2. Targets identified in burn wound fluid at 2 time points 4 days apart.

Targets identified in wound fluid from a H+ burn injury compared to the H- donor graft site of the same subject are shown in Table 3.

Target Protein Name	Phospho Site (Human)	Flag-6B-pool	Best Leads	Z-ratio (6B-pool, 6D)
ZIPK	Pan-specific	0, 0	Priority	2.95
Crystallin aB	Pan-specific	0, 0	Priority	2.58
NME7	Pan-specific	0, 0	Priority	2.05
MEK1	S292	0, 0	Priority	1.89
Rb	S612	0, 0	Priority	1.91
DNAPK	T2609	0, 0	Priority	1.87
MST3	T184	0, 0	Priority	1.80
Cdc25A	Pan-specific	0, 0	Priority	1.88

Akt1 (PKBa)	Y326	0, 0	Priority	1.74
Cdc2L5	Pan-specific	0, 0	Priority	1.77
MEK2 mouse	T394	0, 0	Priority	1.65
p107	Pan-specific	0, 0	Priority	1.59
Abl	Pan-specific	0, 0	Priority	1.61
Cyclin D1	Pan-specific	0, 0	Priority	1.65
ERK1	S74	0, 0	Priority	1.64
Nek7	Pan-specific	0, 0	Priority	1.54
ErbB2	Y1248	0, 0	Priority	1.60
PCTK1	Pan-specific	0, 0	Priority	1.51
Haspin	Pan-specific	0, 0	Priority	1.51
Dok2	Y142	0, 0	Priority	1.53
p21 CDK11	Pan-specific	0, 0	Priority	1.55
HSTK12 (Aurora 2)	Pan-specific	0, 0	Priority	1.55
Kit	Y730	0, 0	Priority	1.47
DUSP12	Pan-specific	0, 0	Priority	1.49
CaMK4	T200	0, 0	Priority	1.56
Fes	Pan-specific	0, 0	Priority	1.51
A6r	Y309	0, 0	Priority	1.53
Csk	Pan-specific	0, 0	Priority	1.45
TTK	Pan-specific	0, 0	Priority	1.47
AK2	Pan-specific	0, 0	Priority	1.49
Bcr	Y177	0, 1	Priority	1.49
GNB2L1	Pan-specific	0, 0	Priority	1.41
B-Raf	Pan-specific	0, 0	Priority	1.47
Cortactin	Y466	0, 0	Priority	1.39
PRKWNK4	Pan-specific	0, 0	Priority	1.38
ILK1	Pan-specific	0, 0	Priority	1.37
MKK3	Y230	0, 0	Priority	1.42
Cyclin E	Pan-specific	0, 0	Priority	1.34
BRSK1	T189	0, 0	Priority	1.42
MEKK2	Pan-specific	0, 0	Priority	1.32
FAK	Y397	0, 0	Priority	1.57
IGF1R	Y1346	0, 0	Priority	1.36
DRAK2	Pan-specific	0, 0	Priority	1.38
SMC1	S957	0, 0	Priority	1.37
Cas-L	Y166	0, 0	Priority	1.37
ALK	Y1507	0, 0	Priority	1.37
Caspase 1	Pan-specific	0, 0	Priority	1.30
Lck	S158	0, 0	Priority	1.29
CamKI	Pan-specific	0, 0	Priority	1.32
Bid	Pan-specific	0, 0	Priority	1.31
BRD2	Pan-specific	0, 0	Priority	1.28
PACSIN1	Pan-specific	0, 0	Priority	1.25
ANKRD3	S438	0, 0	Priority	1.27
Shc1	Y239/Y240	0, 0	Priority	1.22
ERK3	Pan-specific	0, 0	Priority	1.25

TrkA	Pan-specific	0, 0	Priority	1.19
Cyclin B1	Pan-specific	0, 0	Priority	1.29
SHP2	Pan-specific	0, 0	Priority	1.23
AIF	Pan-specific	0, 0	Priority	1.23
Catenin b	Y333	0, 0	Priority	1.16
ERK1/2	Pan-specific	0, 0	Priority	1.22
CAMK2d	Pan-specific	0, 0	Priority	1.22
FGFR1	Y653+Y654	0, 0	Priority	1.30
p38a MAPK	T180+pY182	0, 0	Priority	1.22
Cdc25B	Pan-specific	0, 0	Priority	1.15
NT5E	Pan-specific	0, 0	Priority	1.25
PKCd	Y311	0, 0	Priority	1.18
DUSP11	Pan-specific	0, 0	Priority	1.23
ERK5	T219+Y221	0, 0	Priority	1.18
MEK3/6	S189/193/S207/211	0, 0	Priority	1.11
SPHK2	Pan-specific	0, 0	Priority	1.15
CDC7	T376	0, 0	Priority	1.17
DDR1	Y796+pY797	0, 0	Priority	1.15
ERK4	S186	0, 0	Priority	1.17
AurKB	Pan-specific	0, 0	Priority	1.11
CDK9	T186	0, 0	Priority	1.20
FAS	Pan-specific	0, 0	Priority	1.14
GFAP	S8	0, 0	Priority	1.10
CDK1/2	Y14/Y15	0, 0	Priority	1.08
DGKZ	Pan-specific	0, 0	Priority	1.13
ICK	Y156+T157	0, 0	Priority	1.12
EphA1	Pan-specific	0, 0	Priority	1.09
PKCg	T655	0, 0	Priority	1.06
InsR	Y1189	0, 0	Priority	1.05
SPHK1	Pan-specific	0, 0	Priority	1.05
VIM	Y117	0, 0	Priority	1.05
Pyk2	Pan-specific	0, 0	Priority	1.04
ZIPK	Pan-specific	0, 0	Priority	1.06
IKKa	Pan-specific	0, 0	Priority	1.04
ERK1	T202+Y204	0, 0	Priority	1.10
p18 INK4c	Pan-specific	0, 0	Priority	1.00
B-Raf	S446+S447	0, 0	Priority	1.08
PP2A/Aa/b	Pan-specific	0, 0	Priority	1.03
A-Raf	Pan-specific	0, 0	Priority	1.06
CDK6	Pan-specific	0, 0	Priority	1.01
PKCg	T514	0, 0	Priority	0.99
Dok2	Y142	0, 0	Priority	1.01
Tyro10	Pan-specific	0, 0	Priority	0.95
Histone H3	S10	0, 0	Priority	1.04
Wee1	Pan-specific	0, 0	Priority	1.07
Wip1	Pan-specific	0, 0	Priority	0.92
B-Raf	S729	0, 0	Priority	1.07

PP1/Cb (PP1b)	Pan-specific	0, 0	Priority	0.92
Arrestin b	S412	0, 0	Priority	0.97
DAXX	Pan-specific	0, 0	Priority	0.97
CDK9	S347	0, 0	Priority	0.98
MEK2	Pan-specific	0, 0	Priority	0.98
Lck	Y192	0, 0	Priority	0.88
PPP1R11	Y64	0, 0	Priority	0.91
AAK1	S637	0, 0	Priority	0.95
CDK1	Y19	0, 0	Priority	0.89
Akt1 (PKBa)	Pan-specific	0, 0	Priority	0.95
FAK	Y577	0, 0	Priority	0.88
GSK3a	Y284+Y285	0, 0	Priority	0.91
Met	T1241	0, 0	Priority	0.89
CDK11A	T583	0, 0	Priority	0.98
CaMK4	Pan-specific	0, 0	Priority	0.91
Kit	Y703	0, 0	Priority	0.82
IRS1	Y1179	0, 0	Priority	0.84
ERK1	T207	0, 0	Priority	0.85
VEGF-C	Pan-specific	0, 0	Priority	0.85
PKCe	Pan-specific	0, 0	Priority	0.82
Hsp90b	Pan-specific	0, 0	Priority	0.87
ERK1	Y204+T207	0, 0	Priority	0.86
PKC II	Pan-specific	0, 0	Priority	0.83
MAPKAPK5	T186	0, 0	Priority	0.90
I1PP2A (PHAPI)	Pan-specific	0, 0	Priority	0.87
ATF2	T69+T71	0, 0	Priority	0.80
BLNK	Y84	0, 0	Priority	0.82
PKCg	T514	0, 0	Priority	0.74
p38g MAPK	Pan-specific	0, 0	Priority	0.78
GTF2F1	S385+T389	0, 0	Priority	0.85
COT	Pan-specific	0, 0	Priority	0.82
PRP4K	Y849	0, 0	Priority	0.79
ERK1	Y204	0, 0	Priority	0.73
PKG1b-NT	Pan-specific	0, 0	Priority	0.74
IkB Kinase alpha	Pan-specific	0, 0	Priority	0.77
ErbB4	Pan-specific	0, 0	Priority	0.77
CaMKK	Pan-specific	0, 0	Priority	0.74
COT	Pan-specific	0, 0	Priority	0.74
p27 Kip1	Pan-specific	0, 0	Priority	0.66
MEK1	Pan-specific	0, 0	Priority	0.77
eEF1A1	Y141	0, 0	Priority	0.74
PKCd	Pan-specific	0, 0	Priority	0.68
MEK4	Pan-specific	0, 0	Priority	0.62
CrkL (32H4)	Pan-specific	0, 0	Priority	0.76
Calnexin	Pan-specific	0, 0	Priority	0.75
JAK3	Pan-specific	1, 0	Priority	0.64
Bcl-xS/L	Pan-specific	0, 0	Priority	-1.59

FGFR2	Pan-specific	0, 0	Priority	-1.48
Akt2 (PKBb)	Pan-specific	0, 0	Priority	-1.42
PDK4	Pan-specific	0, 0	Priority	-1.51
STAT5A	Pan-specific	0, 0	Priority	-1.68
Ros	Pan-specific	0, 0	Priority	-1.86
TBK1	S172	0, 0	Priority	-1.89
MEF-2	Pan-specific	0, 0	Priority	-1.99
ErbB2	Pan-specific	0, 0	Priority	-1.86
AurKB	Pan-specific	0, 0	Priority	-2.49
JNK1	Pan-specific	0, 0	Priority	-2.60
PKCI	T555/T563	0, 0	Possible	1.97
ACTA1 (Alpha -actin)	Pan-specific	0, 0	Possible	1.25
Adducin a/g	S662	0, 0	Possible	1.13
FAK	Y576+Y577	0, 0	Possible	1.12
Met	Y1003	0, 0	Possible	1.04
VAV1	Y826	0, 0	Possible	1.02
FAK	Pan-specific	0, 0	Possible	1.01
CSF1R	Y699	0, 0	Possible	0.98
ILK1	Y351	0, 0	Possible	0.75
CDK9	Pan-specific	0, 0	Possible	0.78
p38b MAPK	Pan-specific	0, 0	Possible	0.82
Connexin 43	S367	0, 0	Possible	0.70
Chk1	Pan-specific	0, 0	Possible	0.77
MEK5	Pan-specific	0, 0	Possible	0.77
AMPKa2	S377	0, 0	Possible	0.85
MEK3	Pan-specific	0, 0	Possible	0.68
JAK2	Pan-specific	0, 0	Possible	-1.87
FRS2	Y349	0, 0	Possible	-2.12

Table 3. Targets identified in the burn wound fluid H+ vs donor graft site wound fluid H- in the same subject.

Targets identified in burn wound fluid from a H+ subject at time 0 and 24 hours post are shown in Table 4.

Target Protein Name	Phospho Site (Human)	Best Leads	Z-ratio (1S+1, 1S)
ZIPK	Pan-specific	Priority	3.48
Crystallin aB	Pan-specific	Priority	2.83
PDGFRb	Y716	Priority	2.71
PKCI	T555/T563	Priority	2.50
PDK2	Pan-specific	Priority	2.89
Syk	Pan-specific	Priority	2.49
ErbB2	Pan-specific	Priority	2.39
MYPT1	T696	Priority	1.99

VEGF-C	Pan-specific	Priority	2.18
Ret	Pan-specific	Priority	2.11
Raf1	Pan-specific	Priority	2.20
Nek2	Pan-specific	Priority	2.00
GTF2F1	S385+T389	Priority	2.07
eIF2a	S52	Priority	1.83
PDK4	Pan-specific	Priority	2.15
Lck	Y394	Priority	1.75
AurKB	Pan-specific	Priority	1.83
PKCe	Pan-specific	Priority	1.72
Chk2	Pan-specific	Priority	1.84
BLNK	Y84	Priority	1.63
VGFR2	Pan-specific	Priority	1.85
PKCd	S645	Priority	1.66
Connexin 43	S367	Priority	1.63
Pyk2	Pan-specific	Priority	1.59
CDK9	T186	Priority	1.83
Bak	Pan-specific	Priority	1.53
PKB2-PCT	Pan-specific	Priority	1.87
PDGFRa	Y768	Priority	1.69
MDM2	S166	Priority	1.67
Hpkl	Pan-specific	Priority	1.62
ERK5	Pan-specific	Priority	1.58
PKCg	T655	Priority	1.60
CamKI	Pan-specific	Priority	1.57
mTOR	Pan-specific	Priority	1.84
hsp90b	Pan-specific	Priority	1.75
CREB1	S133	Priority	1.73
CDK6	Pan-specific	Priority	1.54
ErbB3	Y1328	Priority	1.51
KDEL Receptor (KR10)	Pan-specific	Priority	1.54
Hsp70	Pan-specific	Priority	1.75
CrkL (32H4)	Pan-specific	Priority	1.74
Chk1	Pan-specific	Priority	1.59
CaMK2a	T286	Priority	1.72
PDK1	Pan-specific	Priority	1.80
GFAP	S8	Priority	1.47
PKCa	Pan-specific	Priority	1.42
Histone H3	S10	Priority	1.57
Hsp70	Pan-specific	Priority	1.61
NIK	Pan-specific	Priority	1.37
Hsp40	Pan-specific	Priority	1.58
CDK9	S347	Priority	1.53
Caldesmon	S789	Priority	1.38
TrkB	Pan-specific	Priority	1.46
MLK3	T277+S281	Priority	1.45
Nlk	Pan-specific	Priority	1.30

PKA R2a (PKR2)	S98	Priority	1.22
Hsp27	S78	Priority	1.40
ERK4	S186	Priority	1.29
CK1e	Pan-specific	Priority	1.63
Hsp90	Pan-specific	Priority	1.44
TYK2	Pan-specific	Priority	1.40
TBK1	Pan-specific	Priority	1.38
MEK1	Pan-specific	Priority	1.34
Hsp60	Pan-specific	Priority	1.10
Nek2	S171	Priority	1.40
VIM	Y117	Priority	1.10
MST3	T184	Priority	1.13
Crystallin aB	Pan-specific	Priority	1.33
Chk1	S345	Priority	1.18
Hsp105	Pan-specific	Priority	1.00
p38g MAPK	Pan-specific	Priority	1.01
Akt2 (PKBb)	Pan-specific	Priority	1.09
VEGFR2	Y1059	Priority	1.02
PKG1b-NT	Pan-specific	Priority	1.03
CK2a	T360/S362	Priority	1.06
Raf1	Pan-specific	Priority	0.99
PKCh	T655	Priority	0.97
Jun	T91	Priority	0.94
HO2	Pan-specific	Priority	1.19
Cdc25B	Pan-specific	Priority	0.83
YSK4	Pan-specific	Priority	1.28
Syk	Y323	Priority	0.84
IGF1R	Y1346	Priority	0.76
PDK2	Pan-specific	Priority	1.10
MAPKAPK5	T186	Priority	1.01
BRCA1	S1497	Priority	0.72
TYK2	Pan-specific	Priority	0.72
BCKD (BCKDK)	Pan-specific	Priority	1.03
Kit	Y936	Priority	0.73
MAPKAPK2	T222	Priority	0.73
DUSP12	Pan-specific	Priority	0.71
Myc	T58	Priority	0.83
COT	Pan-specific	Priority	0.86
CK2a	Pan-specific	Priority	0.93
PDK1	Pan-specific	Priority	0.97
Grp78	Pan-specific	Priority	0.94
Cofilin 2	S3	Priority	0.85
eIF4G	S1232	Priority	0.60
MLC	S19	Priority	0.59
p38b MAPK	Pan-specific	Priority	0.76
DUSP9	Pan-specific	Priority	-1.43
APG1	Pan-specific	Priority	-1.69

ErbB3	Pan-specific	Priority	-1.30
ERK2	Pan-specific	Priority	-1.36
EGFR	Pan-specific	Priority	-1.64
GRK2	S670	Priority	-1.69
DUSP11	Pan-specific	Priority	-1.56
JAK2	Pan-specific	Priority	-1.73
MKK3	S218	Priority	-1.73
Abl	Pan-specific	Priority	-1.77
Cdc25C	Pan-specific	Priority	-1.74
FGFR2	Pan-specific	Priority	-1.64
PARP1	Pan-specific	Priority	-1.76
DUSP4	Pan-specific	Priority	-1.79
EGFR	Pan-specific	Priority	-1.74
JAK2	Pan-specific	Priority	-1.66
A-Raf	Pan-specific	Priority	-1.90
DUSP7	Pan-specific	Priority	-1.91
DUSP2	Pan-specific	Priority	-1.69
DUSP1 (MKP1)	Pan-specific	Priority	-1.82
MELK	Pan-specific	Priority	-1.94
B-Raf	Pan-specific	Priority	-2.01
Cdc25B	Pan-specific	Priority	-2.07
EGFR	Pan-specific	Priority	-1.99
JAK1	Pan-specific	Priority	-2.19
JAK3	Pan-specific	Priority	-2.21
EGFR	Pan-specific	Priority	-2.34
PRKDC (DNAPK)	Pan-specific	Priority	-2.86
JNK1	Pan-specific	Priority	-4.30
Elk1	S383	Possible	2.01
eIF2a	S52	Possible	1.95
Tau	T231	Possible	1.92
Cyclin B1	S147	Possible	1.37
Lck	Pan-specific	Possible	1.20
VHR	Pan-specific	Possible	1.11
AurKA	Pan-specific	Possible	1.42
S6	S235	Possible	0.91
AurKA	Pan-specific	Possible	1.07
PED15 (PEA15)	S116	Possible	0.96
HDAC4/5/9	S246/259/220	Possible	0.84
Estrongen Receptor	S104	Possible	0.83
Caspase 7	Pan-specific	Possible	0.81
Ros	Pan-specific	Possible	1.12
Lck	S158	Possible	0.81
Tau	T205	Possible	0.81
Jun	S73	Possible	0.87
Calnexin	Pan-specific	Possible	1.08
ERK5	T218+Y220	Possible	0.70
I1PP2A (PHAPI)	Pan-specific	Possible	0.95

LIMK1/2	Y507/T508	Possible	0.68
CSF1R	Y699	Possible	0.60
MEK1	T386	Possible	0.58
Krs-2	Pan-specific	Possible	0.54
MEK4	Pan-specific	Possible	-1.60
Catenin b	Pan-specific	Possible	-2.31
ERK3	Pan-specific	Possible	-2.35
IkBb	Pan-specific	Possible	-2.34

Table 4. Targets identified in H+ burn wound fluid at time 0 and 24 hours later.

The top ten targets from all survey arrays are shown together in Table 5.

H+ vs H- Donor H- vs. Burn H+ H+ Burn time 0 and 24 hrs H+ Burn time 0 and 4 days

Target Protein Name	Z-ratio	Target Protein Name	Z-ratio	Target Protein Name	Z-ratio	Target Protein Name	Z-ratio
Striatin	3.17	ZIPK	2.95	ZIPK	3.48	JNK1	2.58
GSK3a	2.28	Crystallin aB	2.58	Crystallin aB	2.83	FGFR2	2.49
PRKWINK4	2.02	NME7	2.05	PDGFRb	2.71	GADD 153 (CHOP)	2.48
Fes	1.84	MEK1	1.89	PKCI	2.50	WNK3	2.36
MST3	1.72	Rb	1.91	PDK2	2.89	VGFR2	2.32
Crystallin aB	1.63	DNAPK	1.87	Syk	2.49	WNK2	2.26
Src	1.67	MST3	1.80	ErbB2	2.39	PDGFRa	2.27
Hsp27	1.55	Cdc25A	1.88	MYPT1	1.99	MELK	2.15
TYK2	1.45	Akt1 (PKBa)	1.74	VEGF-C	2.18	MEK5	2.11
PACIN1	1.58	Cdc2L5	1.77	Ret	2.11	PP4/A'2	2.04

Table 5. Top 10 Targets identified in survey arrays.

Crystallin aB was present in 3 of arrays in the top 10 list and in the 4th array was identified as a priority target, but not in the top 10. Interestingly, a review of the literature revealed a recent patent discussing the use of this heat shock protein as a potential treatment to prevent burn-related systemic inflammatory response syndrome.

ZipK was identified as a top 10 target in 2 of the arrays and is the pathway it is associated with is shown in Figure 1.

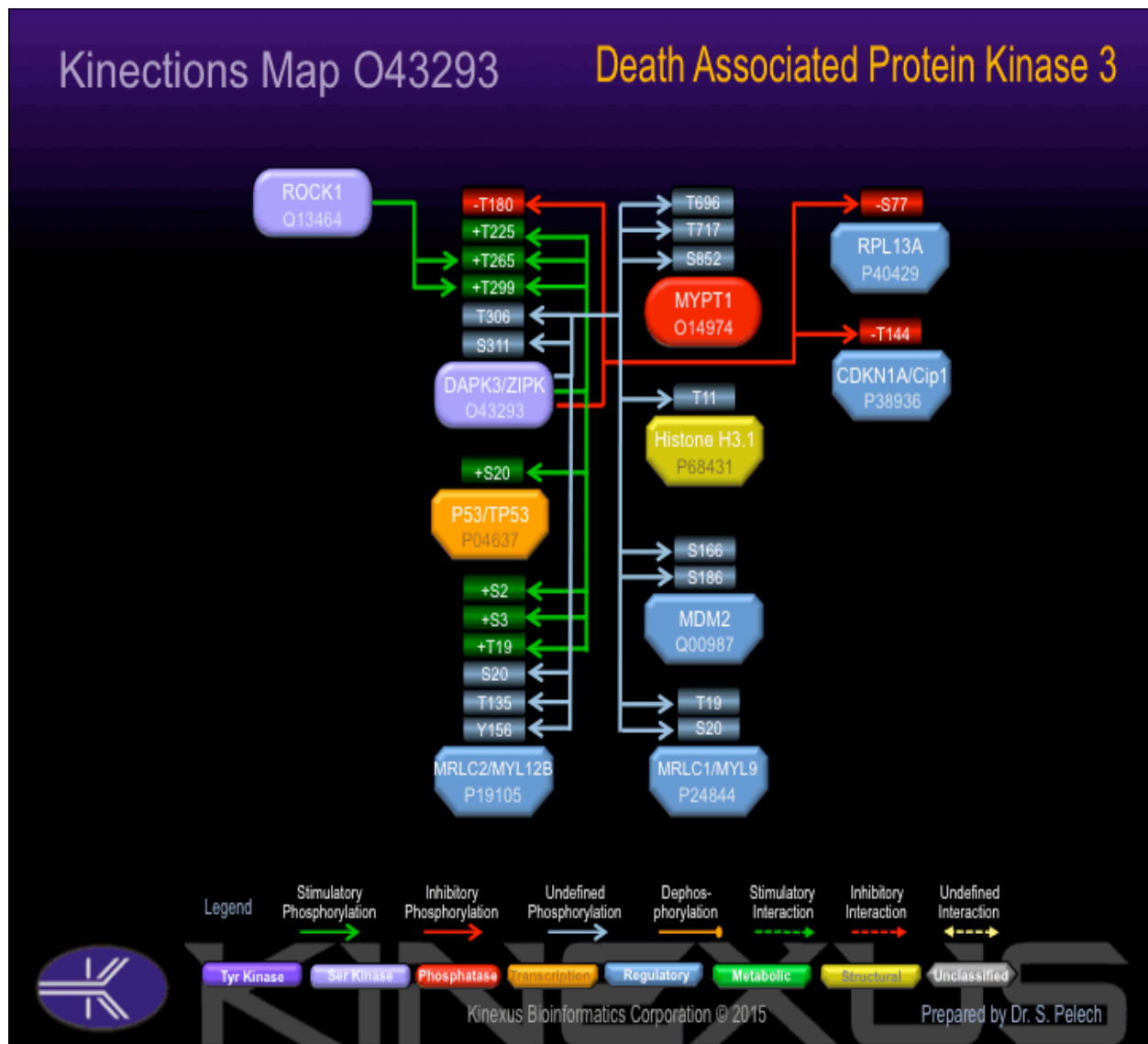


Figure 1. Death Associated Protein Kinase 3 Pathway.

iTRAQ Analysis

iTRAQ labeling quantitative proteomics analysis identified the different expression levels of 4634 proteins in a 6-plex where each channel represented a sample from a single H⁺ individual with multiple samples of burn fluid and donor site fluid from a single H⁺ subject. Channel 1 – burn day 1, channel 2 – donor site day 1, channel 3 - donor site 4 days post harvest, channel 4 -

burn 5 day post graft, channel 5 - burn 7 days post graft, and channel 6 – burn 14 days post graft.
See Appendix A for full results.

The largest differences were between the donor wound and the burn wound on day 1. The difference in injury type and outcome made this comparison integral to understanding beginning to understand the differences in healing between the 2 sites in the same subject, but with different scarring outcomes Table 6.

Target	Ratios: F1: (Channel2, Sample) / (Channel1, Control)	Target	Ratios: F1: (Channel 3, Sample) / (Channel 1, Control)	Target	Ratios: F1: (Channel 4, Sample) / (Channel 1, Control)	Target	Ratios: F1: (Channel5, Sample) / (Channel1, Control)	Target	Ratios: F1: (Channel6, Sample) / (Channel1, Control)
centrosomal protein of 85 kDa isoform 2 [Homo sapiens] PREDICTED :	732.97	histone H2B type 1-L [Homo sapiens]	20.86	matrin- 3 isoform a [Homo sapiens]	17.85	cytoskelet on- associated protein 4 [Homo sapiens]	20.93	interleukin-8 precursor [Homo sapiens]	17.73
centrosomal protein of 85 kDa isoform X1 [Homo sapiens] PREDICTED :	732.97	histone H2B type 1-N [Homo sapiens]	20.86	matrin- 3 isoform b [Homo sapiens]	17.85	SAFB-like transcripti on modulator isoform b [Homo sapiens]	17.04	protein S100-A7-like 2 [Homo sapiens]	17.17
centrosomal protein of 85 kDa isoform X3 [Homo sapiens]	732.97	histone H2B type 1-M [Homo sapiens]	20.86	matrin- 3 isoform c [Homo sapiens] SAFB- like transcri ption modulat or	17.85	SAFB-like transcripti on modulator isoform a [Homo sapiens] PREDICTE D: SAFB- like transcripti on modulator isoform X1 [Homo sapiens] PREDICTE D: SAFB- like transcripti on modulator	17.04	SWISS- PROT:P0267 2 (Bos taurus) Fibrinogen alpha chain precursor	11.78
adenylate kinase isoenzyme 1 [Homo sapiens] PREDICTED :	192.45	histone H2B type 1-H [Homo sapiens]	20.86	SAFB- like transcri ption modulat or	15.13			protein S100-A7 [Homo sapiens]	10.37
adenylate kinase isoenzyme 1 isoform X1 [Homo	192.45	histone H2B type 1-K [Homo sapiens]	20.86		15.13		17.04		

sapiens]				isoform a [Homo sapiens] PREDICTED: SAFB-like transcription modulator isoform X1 [Homo sapiens] PREDICTED: SAFB-like transcription modulator isoform X3 [Homo sapiens]		
PREDICTED : adenylate kinase isoenzyme 1 isoform X3 [Homo sapiens]	192.45	histone H2B type 1-D [Homo sapiens]	20.86		PREDICTED: SAFB-like transcription modulator isoform X4 [Homo sapiens]	17.04
hemoglobin subunit beta [Homo sapiens]	159.90	histone H2B type 1-C/E/F/G/I [Homo sapiens]	20.86		PREDICTED: SAFB-like transcription modulator isoform X5 [Homo sapiens]	17.04
ral GTPase-activating protein subunit alpha-2 [Homo sapiens]	149.10	histone H2B type 2-F isoform a [Homo sapiens]	20.86		PREDICTED: SAFB-like transcription modulator isoform X6 [Homo sapiens]	17.04
PREDICTED : ral GTPase-activating protein subunit alpha-2 isoform X1 [Homo sapiens]	149.10	histone H2B type 2-F isoform b [Homo sapiens]	20.86		PREDICTED: SAFB-like transcription modulator isoform X7 [Homo sapiens]	17.04
PREDICTED : ral GTPase-activating protein subunit alpha-2 isoform X2 [Homo sapiens]	149.10	PREDICTED: histone H2B type 1-D isoform X1 [Homo sapiens]	20.86		eukaryotic translation initiation factor 3 subunit H [Homo sapiens]	11.63
PREDICTED : ral GTPase-	149.10	PREDICTED: histone	20.86			

activating protein subunit alpha-2 isoform X3 [Homo sapiens]		H2B type 2-F isoform X1 [Homo sapiens]	like transcri ption modulat or isoform X7 [Homo sapiens]
		PREDICT ED: histone H2B type 2-F isoform X2 [Homo sapiens]	
peroxiredoxi n-2 [Homo sapiens]	141.98	PREDICT ED: histone H2B type F-S-like [Homo sapiens]	20.86
hemoglobin subunit zeta [Homo sapiens]	126.77	PREDICT ED: histone H2B type F-S-like [Homo sapiens]	20.86
PREDICTED : hemoglobin subunit zeta isoform X1 [Homo sapiens]	126.77	PREDICT ED: histone H2B type F-S-like [Homo sapiens]	20.86
hemoglobin subunit delta [Homo sapiens]	104.43	ribonucle ase pancreati c precursor [Homo sapiens]	15.61
SWISS- PROT:P020 70 (Bos taurus)		histone H2B type 2-E [Homo sapiens]	15.16
Hemoglobin subunit beta	102.06	histone H2B type 1-B [Homo sapiens]	15.16
carbonic anhydrase 1 isoform b [Homo sapiens]	100.17	histone H2B type 1-O [Homo sapiens]	15.16
hemoglobin subunit alpha [Homo sapiens]	86.76	histone H2B type 1-J [Homo sapiens]	15.16
hydroxyacyl glutathione hydrolase, mitochondri al isoform 2 [Homo sapiens]	85.95	histone H2B type 3-B [Homo	15.16
hydroxyacyl glutathione hydrolase, mitochondri	85.95		

al isoform 1 precursor [Homo sapiens] hydroxyacyl glutathione hydrolase, mitochondrial isoform 3 precursor [Homo sapiens]	85.95	sapiens] interleukin-8 precursor [Homo sapiens] pentraxin-related protein PTX3 precursor [Homo sapiens] eosinophil peroxidase preproprotein [Homo sapiens]	13.87
carbonic anhydrase 1 isoform c [Homo sapiens]	80.01		13.56
40S ribosomal protein S19 [Homo sapiens]	71.43		10.89
carbonic anhydrase 1 isoform a [Homo sapiens]	66.88		
hemoglobin subunit gamma-2 [Homo sapiens]	65.65		
hemoglobin subunit gamma-1 [Homo sapiens]	65.18		
alpha-synuclein isoform NACP140 [Homo sapiens]	63.90		
alpha-synuclein isoform NACP112 [Homo sapiens]	63.90		
carbonic anhydrase 2 isoform 2 [Homo sapiens]	58.09		
carbonic anhydrase 3 [Homo sapiens]	54.82		
TREMBL:Q3SX09 (Bos taurus) similar to	53.82		

Table 6. Top differences seen in 6Plex iTRAQ.

The different expression levels of 2422 proteins in the 4-plex compared wound fluid and serum from H+ and H- subjects. Channel 1 was burn fluid pooled from H- subjects, channel 2 was burn fluid pooled from H+ subjects, channel 3 was pooled serum H-, and channel pooled serum from H+ subjects. See Appendix B for full results. Proteins that were reproducibly higher by at least a five-fold expression are given in Table 7.

Description	Ratios: F1: (Channel2, Sample) / (Channel1, Control)	Description	Ratios: F1: (Channel3, Sample) / (Channel1, Control)	Description	Ratios: F1: (Channel4, Sample) / (Channel1, Control)
hemoglobin subunit gamma-1 [Homo sapiens]	15.79	PREDICTED: complement factor I isoform X1 [Homo sapiens]	77.98	PREDICTED: complement factor I isoform X1 [Homo sapiens]	68.08
hemoglobin subunit gamma-2 [Homo sapiens]	12.84	PREDICTED: complement factor I isoform X3 [Homo sapiens]	77.98	PREDICTED: complement factor I isoform X3 [Homo sapiens]	68.08
olfactomedin-4 precursor [Homo sapiens]	8.68	PREDICTED: complement factor I isoform X4 [Homo sapiens]	77.98	PREDICTED: complement factor I isoform X4 [Homo sapiens]	68.08
alpha-N- acetylglucosami nidase precursor [Homo sapiens]	6.90	amyloid beta A4 precursor protein-binding family B member 1 isoform a [Homo sapiens]	43.95	amyloid beta A4 precursor protein- binding family B member 1 isoform a [Homo sapiens]	58.97
PREDICTED: alpha-N- acetylglucosami nidase isoform X1 [Homo sapiens]	6.90	amyloid beta A4 precursor protein-binding family B member 1 isoform b [Homo sapiens]	43.95	amyloid beta A4 precursor protein- binding family B member 1 isoform b [Homo sapiens]	58.97
nuclear ubiquitous	6.20	amyloid beta A4 precursor	43.95	amyloid beta A4 precursor protein-	58.97

casein and cyclin-dependent kinase substrate 1 [Homo sapiens]		protein-binding family B member 1 isoform g [Homo sapiens]		binding family B member 1 isoform g [Homo sapiens]	
PREDICTED: nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 isoform X1 [Homo sapiens]	6.20	amyloid beta A4 precursor protein-binding family B member 1 isoform f [Homo sapiens]	43.95	amyloid beta A4 precursor protein-binding family B member 1 isoform f [Homo sapiens]	58.97
PREDICTED: complement factor I isoform X1 [Homo sapiens]	5.87	amyloid beta A4 precursor protein-binding family B member 1 isoform e [Homo sapiens]	43.95	amyloid beta A4 precursor protein-binding family B member 1 isoform e [Homo sapiens]	58.97
PREDICTED: complement factor I isoform X3 [Homo sapiens]	5.87	amyloid beta A4 precursor protein-binding family B member 1 isoform d [Homo sapiens]	43.95	amyloid beta A4 precursor protein-binding family B member 1 isoform d [Homo sapiens]	58.97
PREDICTED: complement factor I isoform X4 [Homo sapiens]	5.87	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X1 [Homo sapiens]	43.95	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X1 [Homo sapiens]	58.97
serum deprivation-response protein [Homo sapiens]	5.79	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X2 [Homo sapiens]	43.95	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X2 [Homo sapiens]	58.97
(Bos taurus) 81 kDa protein	5.64	amyloid beta A4 precursor	43.95	amyloid beta A4 precursor	58.97

precursor
protein-binding
family B
member 1
isoform X3
[Homo sapiens]

protein-binding family B
member 1 isoform X3
[Homo sapiens]

Table 7 shows the top differences seen in 4Plex iTRAQ.

MULTIPLEXED ARRAY

Serum and burn fluid values of 13 markers implicated in burn hypertrophic scar literature were measured using a multiplexed liquid antibody array. Table 8 below shows a summary of the results for burn (B) or donor (D) site wound fluid. TGF-B1 and HGF had significantly higher values than the other targets.

H+/-	B / D	Time	ANG II	FGF-2	MCP-1	TNF-α	VEGF	IL-12(p40)	HGF	SCF	SDF-1α	IL-4	IL-10	TGF-β1	TGF-β2	TGF-β3
1	D	0	257.5	8	31.5	4.8	80.0	56.1	492.9	36.4	96.2	<8.9	<1.0	8791.2	538.7	<78.1
1	B	0	191.9	7	323.4	5.5	53.2	0	2127.5	70.1	324.1	<8.9	7.6	8123.6	437.1	<78.1
1	B	24	37.4	8.5	52.2	10.8	44.1	95.5	156.7	8.2	104.0	<8.9	<1.0	1223.4	71.1	88.8
1	B	24	2821.6	21.0	6455.1	790.9	1464.5	253.7	6599.5	35.1	111.6	<8.9	1	2556.2	111.5	<78.1
3	B	24	1488.0	6.8	4270.2	113	1490.9	141.6	9624.2	66.0	50.0	<8.9	1	3222.1	138.9	<78.1
3	D	0	215.5	6	5.6	9.3	46.9	2	1105.2	57.4	442.3	<8.9	<1.0	4808.1	166.0	88.7
3	D	24	1597.0	1.7	1560.8	250.2	1939.8	39.9	26108.5	98.2	<6.7	<8.9	4	7858.7	437.1	586.5
3	B	7 d	1062.9	4.5	4394.5	6.3	1049.2	99.4	2580.8	138.4	5	<8.9	19.7	4808.6	247.3	287.9
4	B	24	4724.2	20.8	323.7	19.8	1029.4	253.7	23825.7	21.3	79.4	22.1	12.6	3222.6	328.7	89.0
4	B	48	4913.6	7.0	353.0	8	906.0	261.0	18947.0	2	23.4	<8.9	87.9	3888.9	613.3	188.4
5	B	24	2222.6	6.0	1071.4	69.9	1275.5	56.1	4105.1	45.5	92.1	8	25.2	557.0	84.7	<78.1
5	B	48	3569.9	20.7	1719.1	300.3	2051.0	72.0	15222.2	51.4	139.7	450.4	121.2	4809.0	111.7	<78.1
5	B	24	1087.9	11.8	443.0	13.8	576.2	87.7	3743.4	40.4	133.0	86.4	10.4	223.9	111.8	<78.1
6	B	0	291.4	11.2	37.0	<2.2	505.5	14.3	2169.6	69.0	19.6	<8.9	9.6	3889.0	125.4	<78.1
6	D	0	176.9	5	9.0	7.8	62.5	6	419.8	18.2	126.0	<8.9	<1.0	2223.0	98.2	<78.1
6	D	24	1157.9	0.9	1681.6	138.7	820.2	18.5	12031.8	130.8	24.6	<8.9	<1.0	4809.0	301.6	138.7
6	B	24	556.4	7.8	1246.9	6	1191.4	64.1	8952.9	82.7	55.4	<8.9	20.3	4555.4	206.7	88.4
6	B	24	1734.2	0.9	5434.0	201.7	1130.8	103.3	28259.3	101.3	70.3	<8.9	7.8	4808.6	213.5	89.0
6	B	7 d	5544.2	13.2	744.1	87.4	1232.3	373.8	44959.2	16.6	171.4	50.6	28.2	2889.4	166.0	<78.1
6	B	14 d	2151.5	2.8	5661.1	188.5	1222.2	114.8	28165.7	94.5	104.0	<8.9	2.4	4808.3	233.8	<78.1
7	B	24	1147.7	25.3	2166.3	160.6	1073.0	56.1	5567.9	48.1	446.7	<8.9	25.7	6328.5	220.2	<78.1
7	B	0	45.6	1	903.1	9.3	45.6	87.7	3356.3	72.4	2	<8.9	<1.0	6296.1	247.2	<78.1

7	D	0	201.4	256. 7	33.1	3.2 100 264.	57.2	8.0	595.1	42.9	294. 4	<8.9	<1.0	7689.1	416.8	<78.1
7 9	B	24	307.9	9.5	6746.8	6	1904.1	79.9	4609.7	116.5	139. 7	<8.9	3.1	5865.2	179.6	<78.1
H+ 9	B	24	92.7 1185.	2.5	165.1	3.1	167.0	25.8	1074.9 16790.	3.4	25.0 104.	<8.9	<1.0	557.1	<69.2	<78.1
H+ 9	B	24	8 2080.	15.6	2524.5	51.5	1586.7	56.1	8 26248.	231.7	0	<8.9	24.6	6018.8	267.7	<78.1
H+ 9	B	48	0	14.6	3318.0	56.7	1615.3	18.5	3	45.1	34.4	<8.9	14.5	5141.9	125.4	<78.1
H+ 9	B	72	48.2 1004.	0.7	13.1	2.7	39.1	14.0	410.0 10249.	1.7	8.6	<8.9	<1.0	557.0	<69.2	<78.1
H+ 9	B	4d	0 4001.	2.6	6054.5	16.8	607.3	95.5	5 179. 76952.	62.6	60.6 126.	<8.9	<1.0	3555.8	145.7	<78.1
H+ 9	B	5d	0 129.	3.1	5144.4	13.8	1660.1	4 304.	0	50.3	0	<8.9	7.3	5417.1	206.6	<78.1
H+ 9	B	0	546.6	6	26.2	10.8	196.4	9	815.6	71.3	2 200.	<8.9	<1.0	6819.4	288.0	<78.1
H+ 9	D	0	237.7 2813.	78.3	6.5	9.3 157.	15.5	87.7	377.9 25707.	115.7	4 111.	<8.9	<1.0	557.0	<69.2	<78.1
H+ 9	B	24	9	1.3	3801.1	0	2326.2	14.3	2	83.9	6	<8.9	<1.0	5417.1	532.0	89.0

Table 8. Burn and donor site wound fluid.

Technical Objective 2: Characterize the protein biochemistry in the sera of subjects with burn wounds.

- Analyze sera to determine the proteins present
- Identify trends present in subjects with burns during healing

iTRAQ Analysis

Results from the iTRAQ 4 plex comparing serum from H+ and H- are shown in Table 9. The full results for serum ratios are in Appendix B.

Description	Ratios of Serum+/Serum-
proline-serine-threonine phosphatase-interacting protein 1 [Homo sapiens]	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X1 [Homo sapiens]	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X2 [Homo sapiens]	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X3 [Homo sapiens]	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X4 [Homo sapiens]	24.95
RWD domain-containing protein 1 isoform a [Homo sapiens]	22.23
RWD domain-containing protein 1 isoform b [Homo sapiens]	22.23

signal recognition particle 9 kDa protein isoform 2 [Homo sapiens]	20.71
protein S100-A7 [Homo sapiens]	20.09
nuclease-sensitive element-binding protein 1 [Homo sapiens]	19.85
PREDICTED: nuclease-sensitive element-binding protein 1 isoform X1 [Homo sapiens]	19.85
hepatoma-derived growth factor isoform b [Homo sapiens]	16.64
hepatoma-derived growth factor isoform c [Homo sapiens]	16.64
glycogen [starch] synthase, muscle isoform 1 [Homo sapiens]	16.31
glycogen [starch] synthase, muscle isoform 2 [Homo sapiens]	16.31
histone H1.5 [Homo sapiens]	15.41
PREDICTED: protein S100-A7A isoform X1 [Homo sapiens]	13.25
histone H1.3 [Homo sapiens]	12.67
eukaryotic translation initiation factor 2 subunit 1 [Homo sapiens]	12.31
PREDICTED: nucleobindin-2 isoform X4 [Homo sapiens]	11.58
PREDICTED: nucleobindin-2 isoform X9 [Homo sapiens]	11.58

Table 9. iTRAQ ratios greater than 10 fold for serum from H+ and H- subjects.

MULTIPLEXED ARRAY

Serum values of 13 markers implicated in burn hypertrophic scar literature were measured using a multiplexed liquid antibody array. Table 10 below shows a summary of the results for serum from h+ and H- subjects. The values of TGF-b1 are again significantly greater as they were in the wound fluid samples.

H+/H-	Time Point	ANG II	FGF-2	MCP-1	TNF- α	VEGF	IL-12(p40)	HGF	SCF	SDF-1 α	IL-4	IL-10	TGF-b1	TGF-b2	TGF-b3
1 H+	0	383.3	<0.7	4.6	<2.2	10.9	<7.8	444.7	19.2	<6.7	<8.9	1.3	43277.3	9464.3	287.3
1 H+	At graft – 48 hrs	439.0	2.5	15.5	<2.2	17.5	<7.8	241.1	26.8	<6.7	<8.9	2.1	32883.8	7919.9	88.7
1 H+	5d	447.9	<0.7	6.5	<2.2	21.7	<7.8	292.4	27.0	<6.7	<8.9	<1.0	36830.8	7616.4	188.3
3	0	371.2	<0.7	<0.9	<2.2	30.1	<7.8	290.7	32.7	<6.7	<8.9	30.3	61761.9	10322.1	287.6
3	Graft 72 hrs post	268.2	<0.7	<0.9	<2.2	12.1	<7.8	271.9	43.5	<6.7	<8.9	7.8	40140.0	7847.0	287.9
3	5739.	264.6	<0.7	<0.9	<2.2	41.2	<7.8	239.4	29.9	<6.7	<8.9	2.2	54466.2	10451.1	379.8
5	0	4	<0.7	5.6	21.2	34.9	<7.8	98.5	32.4	29.5	9.0	8.9	38775.8	8060.0	379.7
6 H+	0	200.3	<0.7	14.2	<2.2	57.3	<7.8	132.2	28.1	<6.7	<8.9	7.3	56776.0	10610.5	188.4
7	0	251.6	<0.7	1.0	<2.2	12.3	<7.8	6	55.1	<6.7	<8.9	27.8	21579.5	5482.3	287.2
7	Graft 3 days post	196.2	<0.7	3.6	<2.2	36.5	<7.8	258.3	38.7	<6.7	<8.9	8.7	37591.4	7938.1	379.8
7	103.	261.7	<0.7	7.4	<2.2	84.5	<7.8	644.0	56.2	34.4	<8.9	12.2	38038.6	7228.2	188.4
9 H+	5d	750.9	3	30.2	3	8	7	689.7	7	8	<8.9	<1.0	27104.6	6800.6	287.7
9 H+	Day 8	673.3	124.	58.4	508.	256.	576.	266.0	145.	589.	<8.9	<1.0	29423.5	6343.0	287.5

			5			5	4	5		2	9								
						225.		861.		103.	367.								
9	Day 1	702.1	47.2	33.6	2	72.4	4	273.6	2	5	<8.9	<1.0	37374.3	7367.0	287.9				

Table 10. Serum values for array targets.

Technical Objective 3: Assess the presence of hypertrophic scarring.

- Burn Scar Index (Vancouver Scar Scale) parameters of scar will be assessed
- Identify subjects with hypertrophic scarring burn wounds

This technical objective was completed by trained burn unit research staff over the course of the study. The challenge with the identification of hypertrophic scarring is the time it takes for healing to occur to the point at which scarring can be evaluated. In order to analyze groups and compare between scarring and non-scarring confirmation of outcome is necessary.

Technical Objective 4: Correlate the differences between the sera and burn fluid samples during healing and identify biochemical differences between hypertrophic scarring and non-hypertrophic scarring subjects.

- Correlate the trends in wound and sera biochemistry during healing
- Correlate clinical outcome with biochemistry
- Identify the differences present in sera and wound exudates in samples from subjects with hypertrophic scarring

The clinical outcome and analysis of the data for the survey arrays, iTRAQ, and targeted arrays is ongoing. The evaluation across subject (Subject #6) and across time points was utilized to evaluate the trends seen within individuals and within groups. Manuscripts are in preparation.

Phase II:

Technical Objective 1: Develop a porcine model for burn wounds (second degree - superficial and deep).

- Develop methods to reproducibly induce cutaneous thermal injuries in porcine tissue model.
- Collect wound fluid from thermally injured swine for proteins of clinical interest, based upon those identified in Phase I of this project.

A thermally-injured porcine model was developed for collection of wound fluid and analysis of healing. Deep partial-thickness 2 cm x 2cm (second degree) burns were produced on the paravertebral area of a pig. Aluminum bars were heated to 90°C in a water bath, then dried off and applied to the skin for 40 seconds with all pressure due to gravity alone. It was found that

if the animal did not have a broad enough back, then the bars were not level on the skin and the burns produced were uneven in area and depth. Fluids were collected from all animals.

Technical Objective 2: Characterize the protein biochemistry of porcine wound fluids.

- a. Analyze burn wound fluid by both ELISA and PIXIES.
- b. Compare results from PIXIES with those from ELISA.

PIXIES and ELISA analysis were performed on porcine wound fluids for the following proteins: KGF, IL-1, IL-6, IL-8, IL-12, TNF-alpha. In addition, the PIXIES platform was used to evaluate TGF-alpha and beta, VEGF and EGF detection in untreated biological samples. Spiked biological samples were also assessed to establish correlations. Only KGF, IL-1, IL-6, IL-8 and IL-12 were found in the biological specimens. Detection limits were ≤ 2 pg/ml. These growth factors were differentially expressed in a spatio-temporal pattern consistent with wound healing, and were influenced by treatment. The correlation between ELISA and PIXIES results is 0.952 between 2 (detection limits) and 50 pg/ml. These results reveal the suitability of the PIXIES platform for determining and quantifying the aforementioned protein targets.

Cytokine profiles in unwounded HaCaT supernatants over a selected time interval were determined, as well as profiles in supernatants from wounded HaCaT cells treated with plain or KGF-doped hydrogels, or exogenous KGF. New approaches to membrane design and formulation involving polymeric hydrogel membranes as a simpler approach to preserving protein stability were evaluated. We fabricated patterned HEMA hydrogels and compared the Bovine Serum Albumin uptake and release for these materials as potential platforms for controlling release characteristics by systematically varying surface area. Computational methods were developed to model the degradation process of micro-patterned wound dressings. The degradation kinetics of the micro-patterned structures is controlled by varying their pattern geometry. The biodegradation of micro-patterned structures is modeled geometrically based on Fick's diffusion theory and a modified finite element method. The degradation time and degraded material amount and the protein release rate are determined by the developed computational algorithms.

The results from the experimental analysis of degradation with the computational model were compared and it was found that if the feature size is reduced to nano- or micro-scale, then the degradation follows bulk erosion as soon as blocks are exposed to the solution and lasts in few days, although same polymer shows relatively longer degradation periods due to bigger size.

Technical Objective 3: Evaluate and validate porcine data with those obtained from Phase I studies.

- a. Compare wound fluid biochemistry from thermally injured swine to that from normally-healing human wound fluid from Phase I of the study.

This objective was not completed due to the low enrollment of human subjects and the low amounts of protein present in the burn injuries. The analysis of samples using PIXIES requires a large amount of protein compared to high dimensional multiplexed protein arrays and mass spectrometry shotgun proteomic surveys such as iTRAQ. PIXIES is not the ideal technology for use in samples with low protein or volume. Ultimately, the decision was made to utilize the samples collected to complete the Technical Objectives of Phase 1 of the project where the most benefit would be realized.

4. KEY RESEARCH ACCOMPLISHMENTS:

- Developed methodology to map protein profiles of chronic wounds over time
- Identified proteins unique to healed wounds
- Identified proteins unique to chronic wounds
- Identified proteins differences relative to wound location
- Identified pathways correlated with proteins found in pressure ulcers
- Identified potential biomarkers of healing or lack of healing in chronic wounds
- Identified significant temporal trend of CXCL9 among healed wounds
- Developed porcine thermal injury model system
- Demonstrated viability of PIXIES platform vs. ELISA

- Identified potential targets of interest in burn wound fluid and serum from H+ vs. H-

5. CONCLUSION:

The methodology developed in this work is unique to the field and is being implemented by others in the field and by our team in projects ranging from the identification of proteomic changes related to the development of heterotopic ossification to the changes present in the mucus of skates during healing. It is anticipated that some of the proteins identified will be significant with regard to our understanding of the healing of chronic wounds, as well as serving as potential biomarkers of healing. The proteins identified in this work are being further evaluated as biomarkers of healing in chronic wounds. These biomarkers will serve as the basis of the development of an assay to predict wound outcome and may be the basis for future therapeutics developed to treat chronic wounds. This methodology was applied to the next stage of this project evaluating burn wound for proteomic changes present with scarring or lack of scarring. The identification of differences in survey arrays, targeted arrays, and iTRAQ analysis over time and between wound fluid and serum may be significant with regards to our understanding of the mechanism of hypertrophic scarring. Limited enrollment makes these results preliminary, but future enrollment will work to build this proteomic characterization.

6. PUBLICATIONS, ABSTRACTS, AND PRESENTATIONS

- Abstract “Biochemical Profiles of Healing and Non-Healing Pressure Ulcers”, Edsberg LE, Fries KM, Brogan MS, Wyffels JT, presented as platform presentation at The Symposium on Advanced Wound Care & Wound Healing Society Meeting, April 2008. **(1st Place Oral Abstract Award)***
- Abstract “Wound Surface Biochemistry of Healing and Non-Healing Pressure Ulcers”, Edsberg LE, Fries KM, Brogan MS, Wyffels JT, presented as poster presentation to the World Union of Wound Healing Societies, Third Congress, June 2008
- Invited presentation “Potential Biomarkers of Healing and Non-Healing Pressure Ulcers”, given at the Plenary Session, 11th Annual European Pressure Ulcer Advisory Panel Meeting, Bruges, Belgium, September 2008.*

- Edsberg LE, Wyffels J. Correlation Between Protein Profiles and Tissue Types for Healing and Non-Healing Pressure Ulcers. European Wound Management Association, EWMA, Helsinki, Finland, May 2009.*
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- Wyffels JT, Fries KM, Randall J, Ha D, Lodwig C, Brogan M, Shero M, Edsberg LE. Analysis of chronic pressure ulcer wound fluid using two-dimensional electrophoresis. *International Wound Journal* 2010;7:236-248.
- “Proteins and Pressure Ulcer Outcomes”, Chronic Wounds – Mechanisms and Diagnostics, 2nd Meeting of the Australian Wound and Tissue Repair Society, Perth, Western Australia, March 2010.
- “Translating Pressure Ulcer Research into Clinical Practice”, Plenary Session – Research Translation, Journey into New Frontiers, Australian Wound Management Association, Perth, Western Australia, March 2010.
- Edsberg LE. “Proteomic Approaches for Studying the Phases of Wound Healing”, Invited Chapter, Bioengineering Research of Chronic Wounds. *Studies in Mechanobiology, Tissue Engineering and Biomaterials Series*. Gefen A (ed.), Springer-Verlag Berlin Heidelberg, 2009:343-362.
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- Z. Tao, E.C. Tehan, R.M. Bukowski, Y. Tang, E.L. Shugart, W.G. Holthoff, A.N. Cartwright, A.H. Titus and F.V. Bright, "Templated Xerogels as Platforms for Biomolecule-less Biomolecule Sensors," *Anal. Chim. Acta* 2006, 564, 59-65.
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- L. Yao, L.; K.Y. Yung, V.P. Chodavarapu and F.V. Bright, "CMOS Imaging of Temperature Effects on Pin-Printed Xerogel Sensor Micorarrays," *IEEE Trans. Biomed. Circuit.* 2011, 5, 189-196.
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- N.D. Kraut, J.D. Brattlie, R.E. Deuro, M.M. McGoorty and F.V. Bright*, "High-Throughput Screening System for Creating and Assessing Surface-Modified Porous Silicon," *Appl. Spectrosc.* **2012** in press.

- Z. Zhan, B. Zhou, Z. Fu, F.V. Bright, A.N. Cartwright and A.H. Titus*, “Filterless Optical Oxygen Sensor Based on a CMOS Buried Double Junction Photodiode,” *Sens. Actu : Chem. B* **2012** in press.

7. INVENTIONS, PATENTS AND LICENSES: List all inventions made and patents and licenses applied for and/or issued. Each entry shall include the inventor(s), invention title, patent application number, filing date, patent number if issued, patent issued date, national, or international.

Nothing to report

8. REPORTABLE OUTCOMES: Provide a list of reportable outcomes that have resulted from this research. Reportable outcomes are defined as a research result that is or relates to a product, scientific advance, or research tool that makes a meaningful contribution toward the understanding, prevention, diagnosis, prognosis, treatment and /or rehabilitation of a disease, injury or condition, or to improve the quality of life. This list may include development of prototypes, computer programs and/or software (such as databases and animal models, etc.) or similar products that may be commercialized.

- Developed methodology to identify proteomic changes in tissue, serum, and wound fluid
- Developed porcine burn wound model

9. OTHER ACHIEVEMENTS: This list may include degrees obtained that are supported by this award, development of cell lines, tissue or serum repositories, funding applied for based on work supported by this award, and employment or research opportunities applied for and/or received based on experience/training supported by this award.

- “Role of Bioelectrical and Biochemical Fields in Chronic Non-Healing Wounds of People with Spinal Cord Injury”, was been funded by the Ontario Neurotrauma Foundation for \$211,154 for the period of 1/2008- 1/2010. This project was based on the work supported by the award. This project allowed us to compare the biochemical profiles of pressure ulcers in people with and without spinal cord injuries. (Edsberg LE, Wyffels JT, Ogrin R, Craven C, Houghton P. A pilot study evaluating protein abundance in pressure ulcer fluid from people with and without spinal cord injury. *The Journal of Spinal Cord Medicine* 2014; 38(4).)

- “Integrated Proteomic Analysis and siRNA Therapy for Treatment of Heterotropic Ossification.” a project based on the methodology developed with the award, was funded by the Department of Defense, U.S. Army Medical Research & Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs. Idea Development Award. This project was a new collaboration with investigators from Rutgers University and the U.S. Army Institute of Surgical Research. The project was initiated after meeting at the June 23, 2009 Blood and Blood Safety PLR meeting. Manuscript in preparation.
- “Novel Compounds From Shark and Stingray Epidermal Mucus With Antimicrobial Activity Against Wound Infection Pathogens.” A new project based on the methodology developed with the award was been funded by Department of Defense, U.S. Army Medical Research & Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs. Basic Research Award. This project was a new collaboration with investigators from Mote Marine Laboratory, University of South Florida, and Clemson University. Manuscripts in preparation.

10. REFERENCES: List all references pertinent to the report using a standard journal format (i.e., format used in *Science*, *Military Medicine*, etc.).

11. APPENDICES: Attach all appendices that contain information that supplements, clarifies or supports the text. Examples include original copies of journal articles, reprints of manuscripts and abstracts, a curriculum vitae, patent applications, study questionnaires, and surveys, etc.

Appendix A. iTRAQ_6Plex

Appendix B. iTRAQ_4Plex

APPENDIX A.

Description	Ratios: F1: (Channel2, Sample) / (Channel1, Control)	Ratios: F1: (Channel3, Sample) / (Channel1, Control)	Ratios: F1: (Channel4, Sample) / (Channel1, Control)	Ratios: F1: (Channel5, Sample) / (Channel1, Control)	Ratios: F1: (Channel6, Sample) / (Channel1, Control)
actin, alpha skeletal muscle [Homo sapiens]	4.40	0.98	1.27	1.53	0.88
actin, aortic smooth muscle [Homo sapiens]	2.79	0.94	0.49	0.31	0.69
actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sapiens]	2.79	0.94	0.49	0.31	0.69
alpha-actinin-2 isoform 1 [Homo sapiens]	0.91	0.96	2.35	1.74	0.90
adenylate kinase isoenzyme 1 [Homo sapiens]	192.45	0.88	0.82	0.38	0.92

arachidonate 5-lipoxygenase isoform 1 [Homo sapiens]	2.79	0.83	0.88	1.18	0.90
annexin A4 [Homo sapiens]	2.17	1.59	1.21	1.76	1.78
annexin A5 [Homo sapiens]	2.02	2.46	2.45	2.38	2.27
annexin A7 isoform 1 [Homo sapiens]	5.87	1.44	1.34	1.00	1.25
NEDD8-activating enzyme E1 regulatory subunit isoform a [Homo sapiens]	2.34	1.22	1.37	1.64	1.20
adenine phosphoribosyltransferase isoform a [Homo sapiens]	3.26	2.08	0.93	0.74	0.83
ADP-ribosylation factor 1 [Homo sapiens]	1.64	0.99	0.70	0.61	0.79
ADP-ribosylation factor 4 [Homo sapiens]	11.78	1.53	2.73	3.11	2.41
V-type proton ATPase subunit C 1 [Homo sapiens]	0.75	0.91	1.65	2.11	0.94
barrier-to-autointegration factor [Homo sapiens]	4.99	1.42	2.19	1.91	2.07
biglycan preproprotein [Homo sapiens]	15.50	0.79	0.64	0.52	0.97
flavin reductase (NADPH) [Homo sapiens]	31.55	0.92	0.77	0.41	0.96
complement component 1 Q subcomponent-binding protein, mitochondrial precursor [Homo sapiens]	1.18	1.36	4.67	1.87	2.44
calpain small subunit 1 [Homo sapiens]	2.02	0.91	0.89	0.62	0.98
caspase-4 isoform alpha precursor [Homo sapiens]	0.62	1.38	2.16	1.36	1.94
T-complex protein 1 subunit zeta isoform a [Homo sapiens]	4.99	1.26	1.34	2.24	1.63
clathrin light chain A isoform a [Homo sapiens]	1.47	0.76	0.79	2.51	0.75
collagen alpha-1(III) chain preproprotein [Homo sapiens]	0.80	3.32	2.00	0.50	1.82
carboxypeptidase N catalytic chain precursor [Homo sapiens]	7.08	1.96	0.88	0.28	0.74
protein CREG1 precursor [Homo sapiens]	2.46	0.81	0.75	0.61	0.92
mitogen-activated protein kinase 14 isoform 1 [Homo sapiens]	4.16	1.28	1.47	1.39	2.30
casein kinase II subunit alpha isoform a [Homo sapiens]	20.10	1.24	0.75	0.84	1.83
cystatin-B [Homo sapiens]	2.76	2.45	1.56	1.57	2.21
cathepsin D preproprotein [Homo sapiens]	1.82	3.59	3.86	3.19	2.02
protein DEK isoform 1 [Homo sapiens]	0.77	2.45	0.82	0.98	1.23
D-dopachrome decarboxylase [Homo sapiens]	5.20	1.96	0.83	0.85	0.92
thymidine phosphorylase isoform 1 proprotein [Homo sapiens]	1.41	0.99	1.54	0.85	2.01
elongation factor 1-alpha 1 [Homo sapiens]	1.64	1.28	1.88	2.09	1.23
elongation factor 1-alpha 2 [Homo sapiens]	1.18	1.29	2.07	3.30	1.40
elongation factor 1-beta [Homo sapiens]	5.15	2.45	2.18	2.70	1.48
elongation factor 1-gamma [Homo sapiens]	1.28	1.19	0.99	0.95	2.76
elongation factor 2 [Homo sapiens]	2.00	0.96	1.24	1.18	1.28
eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens]	1.44	1.18	1.87	1.98	2.60
eukaryotic translation initiation factor 3 subunit A [Homo sapiens]	2.66	0.93	0.89	0.97	0.75
eukaryotic translation initiation factor 3 subunit I [Homo sapiens]	1.00	2.01	1.34	1.27	1.21
eukaryotic translation initiation factor 3 subunit H [Homo sapiens]		4.11	5.19	11.63	5.16
eukaryotic translation initiation factor 3 subunit F [Homo sapiens]	2.79	1.70	2.38	2.67	1.43
eukaryotic translation initiation factor 3 subunit E [Homo sapiens]	10.40	2.34	1.73	1.38	2.35
eukaryotic initiation factor 4A-I isoform 1 [Homo sapiens]	2.19	1.00	1.48	1.56	1.27
eukaryotic translation initiation factor 4E isoform 1 [Homo sapiens]	5.87	1.26	2.15	3.30	1.30
eosinophil peroxidase preproprotein [Homo sapiens]		10.89	1.93	3.91	5.14
immunoglobulin alpha Fc receptor isoform a precursor	7.95	1.53	0.95	0.55	0.92

[Homo sapiens]

farnesyl pyrophosphate synthase isoform a [Homo sapiens]	4.38	1.17	3.59	5.56	2.71
tyrosine-protein kinase Fes/Fps isoform 1 [Homo sapiens]	2.33	2.59	0.81	0.51	0.92
fibrinogen alpha chain isoform alpha-E preproprotein [Homo sapiens]	1.41	1.75	1.46	0.93	2.07
peptidyl-prolyl cis-trans isomerase FKBP4 [Homo sapiens]	3.34	0.94	0.91	0.75	0.93
protein flightless-1 homolog isoform 1 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Homo sapiens]	1.34	0.85	2.16	2.46	0.83
X-ray repair cross-complementing protein 6 isoform 1 [Homo sapiens]	1.24	1.62	2.47	0.98	2.39
rab GDP dissociation inhibitor alpha [Homo sapiens]	2.08	1.17	1.68	1.63	1.36
starch-binding domain-containing protein 1 [Homo sapiens]	1.47	2.08	0.84	0.69	0.92
gamma-glutamyl hydrolase precursor [Homo sapiens]	0.77	1.26	2.35	0.81	1.26
glutamate--cysteine ligase regulatory subunit [Homo sapiens]	0.80	0.97	0.55	0.35	0.64
glutaredoxin-1 [Homo sapiens]	1.57	1.90	1.43	1.34	1.23
GDP-mannose 4,6 dehydratase isoform 1 [Homo sapiens]	2.19	0.96	2.09	2.06	1.39
GMP synthase [glutamine-hydrolyzing] [Homo sapiens]	2.49	1.19	2.51	3.62	2.30
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
N-acetylglucosamine-6-sulfatase precursor [Homo sapiens]	0.57	1.28	1.60	1.39	2.45
aspartate aminotransferase, cytoplasmic [Homo sapiens]	2.58	1.00	0.64	0.49	0.91
histone H2AX [Homo sapiens]	2.02	2.05	0.70	0.30	0.79
histone H2A.Z [Homo sapiens]	0.41	3.48	0.91	1.26	1.28
histone H2B type 1-L [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
histone H2B type 1-N [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
histone H2B type 1-M [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
histone H2B type 1-H [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
histone H2B type 2-E [Homo sapiens]	0.57	15.16	1.27	0.29	4.54
histone H3.1 [Homo sapiens]	1.64	3.86	0.88	0.41	2.10
histone H4 [Homo sapiens]	0.80	6.81	1.43	0.45	2.35
trifunctional enzyme subunit beta, mitochondrial isoform 1 precursor [Homo sapiens]	0.43	0.81	1.00	0.43	4.36
hemoglobin subunit alpha [Homo sapiens]	86.76	0.89	0.97	0.23	1.35
hemoglobin subunit beta [Homo sapiens]	159.90	0.95	1.38	0.24	1.42
hemoglobin subunit delta [Homo sapiens]	104.43	0.89	1.18	0.28	1.20
heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]	1.31	2.20	1.29	1.34	2.30
heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2 [Homo sapiens]	0.83	0.93	1.28	1.47	1.35
hypoxanthine-guanine phosphoribosyltransferase [Homo sapiens]	11.07	2.08	1.38	1.30	2.16
histidine-rich glycoprotein precursor [Homo sapiens]	0.43	0.73	0.37	0.22	0.61
dnaJ homolog subfamily A member 1 [Homo sapiens]	0.33	1.58	1.82	2.14	1.56
heat shock protein beta-1 [Homo sapiens]	17.52	0.39	0.49	0.07	0.46
10 kDa heat shock protein, mitochondrial [Homo sapiens]	0.69	1.40	1.98	2.51	1.21
interferon regulatory factor 8 [Homo sapiens]	1.41	0.94	0.44	0.24	0.57
interleukin-18 isoform 1 proprotein [Homo sapiens]	1.41	1.00	2.47	1.31	0.94
polyadenylate-binding protein 4 isoform 2 [Homo sapiens]	0.77	2.32	1.47	1.65	1.39

voltage-gated potassium channel subunit beta-2 isoform 1 [Homo sapiens]	0.88	1.98	1.91	2.37	1.86
kininogen-1 isoform 2 precursor [Homo sapiens]	0.19	0.54	0.28	0.08	0.30
importin subunit alpha-3 [Homo sapiens]	2.58	0.97	1.21	0.89	1.17
lumican precursor [Homo sapiens]	2.83	2.08	0.29	0.12	0.25
protein mago nashi homolog [Homo sapiens]	2.34	1.59	2.33	3.87	1.61
NAD-dependent malic enzyme, mitochondrial isoform 1 precursor [Homo sapiens]	0.67	2.59	0.99	0.85	0.93
macrophage migration inhibitory factor [Homo sapiens]	5.15	1.87	2.76	6.81	2.71
stromelysin-2 preproprotein [Homo sapiens]	3.43	4.99	1.18	1.50	3.47
interstitial collagenase isoform 1 preproprotein [Homo sapiens]	1.18	4.56	1.18	0.65	1.63
stromelysin-1 preproprotein [Homo sapiens]	1.21	3.77	0.84	0.88	2.77
moesin [Homo sapiens]	0.64	2.20	1.24	1.51	1.25
protein phosphatase 1 regulatory subunit 12A isoform a [Homo sapiens]	0.43	0.91	0.91	1.38	1.81
nucleoside diphosphate kinase B isoform a [Homo sapiens]	4.02	1.62	2.40	2.38	2.19
oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens]	0.62	1.26	0.71	0.35	2.68
platelet-activating factor acetylhydrolase IB subunit beta isoform a [Homo sapiens]	4.99	0.82	0.93	1.25	0.96
serine/threonine-protein kinase PAK 3 isoform a [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
phosphatidylethanolamine-binding protein 1 preproprotein [Homo sapiens]	7.36	1.26	1.58	1.43	1.20
proliferating cell nuclear antigen [Homo sapiens]	1.41	1.26	2.29	0.94	1.23
pyridoxal kinase [Homo sapiens]	1.18	0.97	0.98	0.95	1.74
properdin precursor [Homo sapiens]	0.19	0.94	0.53	0.45	0.92
phosphoglycerate mutase 1 [Homo sapiens]	2.79	1.25	1.34	1.39	1.17
phosphoglycerate kinase 1 [Homo sapiens]	1.79	2.08	1.43	1.74	1.34
elafin preproprotein [Homo sapiens]	0.19	1.68	1.21	1.99	4.55
dynein light chain 1, cytoplasmic [Homo sapiens]	1.18	0.84	0.95	0.94	0.79
plasminogen isoform 1 precursor [Homo sapiens]	0.28	0.53	0.38	0.16	0.68
proteolipid protein 2 [Homo sapiens]	0.54	1.51	1.68	1.68	1.18
protein PML isoform 6 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
platelet basic protein preproprotein [Homo sapiens]	20.02	0.46	0.38	0.18	0.62
protein phosphatase 1B isoform 1 [Homo sapiens]	0.57	0.88	0.76	0.87	0.96
serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 1 [Homo sapiens]	0.88	1.62	0.75	0.61	0.78
serine/threonine-protein phosphatase PP1-gamma catalytic subunit isoform 1 [Homo sapiens]	0.41	0.91	0.48	0.34	0.52
protein phosphatase 1 regulatory subunit 7 isoform 1 [Homo sapiens]	1.61	1.19	2.29	1.44	1.23
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform isoform 1 [Homo sapiens]	1.64	0.89	2.26	1.51	0.99
calcineurin subunit B type 1 [Homo sapiens]	0.91	0.85	0.68	0.53	0.67
serine/threonine-protein phosphatase 6 catalytic subunit isoform b [Homo sapiens]	2.08	1.40	0.84	1.52	0.80
cAMP-dependent protein kinase catalytic subunit alpha isoform 1 [Homo sapiens]	0.91	0.69	0.78	1.00	0.80
cAMP-dependent protein kinase catalytic subunit beta isoform 2 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
5'-AMP-activated protein kinase subunit gamma-1 isoform 1 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
mitogen-activated protein kinase 10 isoform 1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08

mitogen-activated protein kinase 13 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 6 [Homo sapiens]	2.11	1.96	2.07	2.33	2.05
mitogen-activated protein kinase 8 isoform alpha1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
vitamin K-dependent protein C preproprotein [Homo sapiens]	0.43	0.43	0.30	0.13	0.23
ribose-phosphate pyrophosphokinase 1 isoform 1 [Homo sapiens]	9.70	0.89	0.70	0.68	0.83
ribose-phosphate pyrophosphokinase 2 isoform 2 [Homo sapiens]	9.42	0.83	0.70	0.69	0.84
phosphoribosyl pyrophosphate synthase-associated protein 2 isoform 1 [Homo sapiens]	6.63	1.41	1.45	1.37	0.96
trypsin-2 preproprotein [Homo sapiens]	1.61	0.48	0.20	0.13	0.32
proteasome subunit alpha type-1 isoform 2 [Homo sapiens]	3.47	1.29	2.16	2.06	1.63
proteasome subunit alpha type-2 [Homo sapiens]	3.43	1.31	1.88	1.40	1.59
proteasome subunit alpha type-3 isoform 1 [Homo sapiens]	5.56	1.58	2.81	1.66	2.08
proteasome subunit alpha type-4 isoform 1 [Homo sapiens]	3.65	1.28	1.69	1.43	1.44
proteasome subunit alpha type-7 [Homo sapiens]	4.65	1.21	1.93	1.53	1.54
proteasome subunit beta type-10 precursor [Homo sapiens]	1.44	1.21	1.43	1.40	1.45
proteasome subunit beta type-1 [Homo sapiens]	2.15	2.71	1.36	1.36	0.90
proteasome subunit beta type-2 isoform 1 [Homo sapiens]	3.34	2.08	1.48	0.49	0.63
proteasome subunit beta type-5 isoform 1 [Homo sapiens]	4.50	1.90	0.76	0.45	2.68
proteasome subunit beta type-7 proprotein [Homo sapiens]	4.07	1.39	1.27	0.69	1.26
proteasome subunit beta type-9 proprotein [Homo sapiens]	1.44	1.55	2.68	0.79	1.39
26S protease regulatory subunit 7 isoform 1 [Homo sapiens]	3.90	0.76	0.65	0.70	0.67
26S proteasome non-ATPase regulatory subunit 10 isoform 1 [Homo sapiens]	10.65	0.95	1.41	2.44	1.24
26S proteasome non-ATPase regulatory subunit 12 isoform 1 [Homo sapiens]	4.40	2.08	2.17	3.69	1.33
polypyrimidine tract-binding protein 1 isoform a [Homo sapiens]	1.57	1.51	1.58	1.91	1.45
ras-related protein Rab-13 isoform 1 [Homo sapiens]	1.61	1.51	1.21	1.20	1.42
ras-related protein Rab-2A isoform a [Homo sapiens]	0.52	1.90	3.91	3.36	1.96
ras-related protein Rab-5B isoform 1 [Homo sapiens]	0.77	1.58	2.79	4.19	1.35
ras-related C3 botulinum toxin substrate 2 [Homo sapiens]	0.50	0.85	1.19	2.00	2.08
UV excision repair protein RAD23 homolog B isoform 1 [Homo sapiens]	2.27	0.96	1.62	2.17	2.01
ran-specific GTPase-activating protein isoform 2 [Homo sapiens]	15.50	0.70	2.26	1.24	0.78
histone-binding protein RBBP7 isoform 2 [Homo sapiens]	2.00	1.19	1.74	0.83	0.97
radixin isoform 2 [Homo sapiens]	3.30	0.91	0.61	0.35	0.66
60S ribosomal protein L12 [Homo sapiens]	2.34	0.99	0.90	0.71	1.82
60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]	1.18	1.46	2.28	1.26	1.42
60S acidic ribosomal protein P2 [Homo sapiens]	2.08	1.63	2.29	1.37	2.16
40S ribosomal protein S16 [Homo sapiens]	5.04	2.45	2.29	1.30	1.29
40S ribosomal protein S19 [Homo sapiens]	71.43	1.45	2.81	3.52	2.73
40S ribosomal protein S25 [Homo sapiens]	2.49	0.93	1.43	1.43	1.35
40S ribosomal protein S3a isoform 1 [Homo sapiens]	4.99	1.17	2.07	2.53	1.75
40S ribosomal protein S4, X isoform X isoform [Homo sapiens]	1.93	0.93	2.16	1.72	1.26

sapiens]					
40S ribosomal protein S7 [Homo sapiens]	0.28	1.80	1.34	0.89	1.19
40S ribosomal protein S8 [Homo sapiens]	0.35	0.64	0.37	0.44	0.50
ruvB-like 1 [Homo sapiens]	2.66	0.91	1.72	1.22	0.90
protein S100-A10 [Homo sapiens]	7.02	0.34	0.87	0.33	0.67
protein S100-A4 [Homo sapiens]	5.72	0.94	1.27	2.15	1.80
protein S100-A9 [Homo sapiens]	0.66	1.70	2.30	2.77	2.35
ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	1.31	0.93	2.69	2.81	1.82
serine/arginine-rich splicing factor 3 [Homo sapiens]	0.66	0.77	0.71	1.37	0.87
small glutamine-rich tetratricopeptide repeat-containing protein alpha [Homo sapiens]	10.14	0.91	0.92	0.77	0.90
SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	4.38	1.51	1.68	1.42	2.76
alpha-synuclein isoform NACP140 [Homo sapiens]	63.90	0.91	0.81	0.33	0.84
fascin [Homo sapiens]	6.44	0.83	0.85	0.50	1.24
small nuclear ribonucleoprotein-associated proteins B and B' isoform B [Homo sapiens]	2.79	2.82	5.60	7.21	2.69
small nuclear ribonucleoprotein E [Homo sapiens]	8.96	1.27	1.26	0.54	1.42
small nuclear ribonucleoprotein F [Homo sapiens]	0.14	1.51	2.46	2.68	1.47
small nuclear ribonucleoprotein G [Homo sapiens]	6.25	2.05	3.57	4.14	2.60
sorting nexin-3 isoform a [Homo sapiens]	5.15	0.99	1.19	1.88	0.97
superoxide dismutase [Cu-Zn] [Homo sapiens]	25.60	2.45	1.53	0.83	1.43
sorcin isoform A [Homo sapiens]	14.12	0.75	0.66	0.69	1.61
signal recognition particle 9 kDa protein isoform 2 [Homo sapiens]	0.62	1.26	1.27	2.09	1.20
sulfotransferase 1A2 [Homo sapiens]	0.46	0.77	0.64	0.84	2.53
transforming growth factor-beta-induced protein ig-h3 precursor [Homo sapiens]	0.80	1.26	0.75	0.34	1.40
metalloproteinase inhibitor 1 precursor [Homo sapiens]	1.34	3.36	1.51	0.69	1.21
troponin C, skeletal muscle [Homo sapiens]	0.88	1.26	0.98	2.48	1.72
triosephosphate isomerase isoform 1 [Homo sapiens]	2.02	1.21	1.43	1.25	1.39
tropomyosin alpha-4 chain isoform 2 [Homo sapiens]	2.76	0.87	1.21	0.77	0.97
translationally-controlled tumor protein isoform 2 [Homo sapiens]	1.28	1.28	2.68	3.39	1.94
endoplasmic precursor [Homo sapiens]	0.75	1.34	1.72	0.85	0.94
GDP-L-fucose synthase [Homo sapiens]	12.66	0.98	1.87	0.90	2.01
transthyretin precursor [Homo sapiens]	0.66	0.57	0.25	0.15	0.53
ubiquitin-60S ribosomal protein L40 precursor [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
ubiquitin-conjugating enzyme E2 L3 isoform 1 [Homo sapiens]	2.38	0.94	1.27	1.56	1.82
NEDD8-conjugating enzyme Ubc12 [Homo sapiens]	1.68	1.40	1.43	1.89	1.17
ubiquitin-conjugating enzyme E2 N [Homo sapiens]	5.77	1.17	2.16	1.82	1.57
ubiquitin-conjugating enzyme E2 variant 2 [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
vasodilator-stimulated phosphoprotein [Homo sapiens]	0.28	0.91	1.79	2.49	1.35
prefoldin subunit 3 [Homo sapiens]	2.00	1.25	1.21	0.92	0.92
wiskott-Aldrich syndrome protein [Homo sapiens]	2.70	0.82	0.81	0.42	0.81
exportin-1 [Homo sapiens]	4.16	1.26	0.90	1.43	1.61
tyrosine--tRNA ligase, cytoplasmic [Homo sapiens]	2.70	2.08	1.75	2.76	1.68
14-3-3 protein beta/alpha [Homo sapiens]	0.91	1.18	1.56	1.52	2.76
14-3-3 protein eta [Homo sapiens]	0.75	2.71	1.71	2.53	1.45
zyxin [Homo sapiens]	0.67	1.62	0.77	1.51	0.68

catalase [Homo sapiens]	9.52	1.21	1.34	0.94	1.21
acetyl-CoA acetyltransferase, mitochondrial precursor [Homo sapiens]	0.75	0.82	1.80	0.88	1.48
adenylosuccinate lyase isoform a [Homo sapiens]	3.52	0.88	0.58	0.56	0.70
angiotensinogen preproprotein [Homo sapiens]	0.66	2.08	0.52	0.27	0.53
fructose-bisphosphate aldolase A isoform 1 [Homo sapiens]	1.51	1.73	2.49	0.98	1.61
bleomycin hydrolase [Homo sapiens]	1.89	1.19	1.39	0.81	2.56
biotinidase isoform 3 [Homo sapiens]	0.06	0.49	0.17	0.13	0.24
tyrosine-protein kinase BTK isoform 1 [Homo sapiens]	0.39	0.79	0.31	0.18	0.53
complement component C8 alpha chain precursor [Homo sapiens]	0.31	2.20	0.61	0.38	0.61
carbonic anhydrase 2 isoform 1 [Homo sapiens]	38.45	0.80	0.71	0.28	0.89
AP-2 complex subunit beta isoform b [Homo sapiens]	1.89	1.19	0.83	1.77	0.83
ceruloplasmin precursor [Homo sapiens]	0.56	1.24	0.52	0.32	0.85
fatty acid-binding protein, epidermal [Homo sapiens]	0.91	0.99	1.21	1.24	2.13
fumarylacetoacetase [Homo sapiens]	4.60	2.08	1.44	1.19	1.21
epididymal secretory glutathione peroxidase isoform 1 precursor [Homo sapiens]	0.18	1.44	0.75	0.39	0.92
keratin, type I cytoskeletal 17 [Homo sapiens]	0.83	0.88	0.94	0.62	0.93
mannose-binding protein C precursor [Homo sapiens]	0.64	2.08	1.00	0.79	1.22
platelet-activating factor acetylhydrolase IB subunit alpha [Homo sapiens]	1.61	1.26	1.65	0.83	1.36
pyrin isoform 1 [Homo sapiens]	0.33	0.70	0.61	1.97	0.68
myeloperoxidase precursor [Homo sapiens]	0.77	2.52	0.90	1.69	1.70
nucleoside diphosphate kinase A isoform b [Homo sapiens]	2.33	0.89	0.95	0.88	0.84
pterin-4-alpha-carbinolamine dehydratase isoform 1 [Homo sapiens]	1.41	0.92	0.78	0.70	0.94
serotransferrin precursor [Homo sapiens]	0.25	0.66	0.24	0.12	0.45
phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	0.26	0.85	0.41	0.20	0.46
lysozyme C precursor [Homo sapiens]	0.67	2.29	2.07	1.63	1.89
low molecular weight phosphotyrosine protein phosphatase isoform c [Homo sapiens]	9.33	1.21	0.77	0.75	2.45
actin-like protein 6A isoform 1 [Homo sapiens]	0.16	0.91	1.80	2.74	0.96
myc box-dependent-interacting protein 1 isoform 8 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
rho-related GTP-binding protein RhoB precursor [Homo sapiens]	2.27	1.19	0.81	0.57	0.92
rho GTPase-activating protein 1 [Homo sapiens]	1.93	0.89	0.76	0.63	0.73
rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens]	1.37	1.00	1.62	2.11	1.22
beta-arrestin-2 isoform 1 [Homo sapiens]	1.31	1.25	1.44	2.25	1.45
V-type proton ATPase subunit G 1 [Homo sapiens]	0.69	0.81	1.37	2.59	0.90
beta-2-microglobulin precursor [Homo sapiens]	0.69	2.05	0.76	0.66	0.89
mitotic checkpoint protein BUB3 isoform a [Homo sapiens]	2.00	1.24	0.56	0.37	0.90
calreticulin precursor [Homo sapiens]	0.95	2.05	3.41	1.82	1.43
clathrin heavy chain 1 isoform 1 [Homo sapiens]	1.76	0.85	0.90	2.01	0.78
calponin-2 isoform a [Homo sapiens]	0.77	1.90	1.78	2.41	1.62
coatamer subunit beta' [Homo sapiens]	2.00	1.00	0.90	0.73	1.27
di-N-acetylchitobiase precursor [Homo sapiens]	1.64	1.65	1.27	1.22	1.61
spliceosome RNA helicase DDX39B [Homo sapiens]	1.00	1.73	0.62	0.41	0.63
death-associated protein 1 isoform 2 [Homo sapiens]		2.18	2.10	1.78	1.87
serine/threonine-protein kinase 17B [Homo sapiens]	0.35	0.84	1.29	3.74	1.61

eukaryotic translation initiation factor 2 subunit 1 [Homo sapiens]	0.98	0.98	0.87	0.79	0.97
protein 4.1 isoform 6 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
enhancer of rudimentary homolog [Homo sapiens]	0.67	1.96	0.84	0.65	0.90
protein disulfide-isomerase A4 precursor [Homo sapiens]	0.80	1.41	2.07	1.54	1.57
phenylalanine--tRNA ligase alpha subunit [Homo sapiens]	4.12	0.75	0.53	0.94	0.60
flap endonuclease 1 [Homo sapiens]	0.98	0.91	0.75	0.71	0.96
glia maturation factor gamma [Homo sapiens]	0.77	0.93	1.48	2.69	1.65
glia maturation factor beta [Homo sapiens]	2.70	0.81	0.90	0.89	0.87
glutathione S-transferase omega-1 isoform 1 [Homo sapiens]	3.26	1.24	1.61	1.78	1.34
core histone macro-H2A.1 isoform 2 [Homo sapiens]	0.66	0.98	0.89	0.64	0.76
hyaluronan-binding protein 2 isoform 1 preproprotein [Homo sapiens]	0.33	0.74	0.33	0.22	0.53
hepatoma-derived growth factor isoform a [Homo sapiens]	0.52	1.36	1.52	2.49	1.80
hepatocyte growth factor-regulated tyrosine kinase substrate [Homo sapiens]	10.46	0.82	0.46	0.42	0.53
peroxiredoxin-6 [Homo sapiens]	24.40	0.83	2.47	2.51	0.99
kinesin-1 heavy chain [Homo sapiens]	0.77	0.92	1.43	1.94	0.94
asparagine--tRNA ligase, cytoplasmic [Homo sapiens]	8.60	1.00	2.79	5.14	1.40
peptidyl-prolyl cis-trans isomerase B precursor [Homo sapiens]	1.21	1.35	1.78	1.45	1.51
cAMP-dependent protein kinase type II-alpha regulatory subunit [Homo sapiens]		0.41	1.60	1.23	1.91
proteasome subunit beta type-8 isoform E1 proprotein [Homo sapiens]	0.88	0.91	0.76	0.73	0.75
ras-related protein Rab-11A isoform 1 [Homo sapiens]	0.95	1.56	1.18	2.13	1.29
ras-related protein Rab-1A isoform 1 [Homo sapiens]	0.83	2.59	1.80	2.55	1.18
eukaryotic peptide chain release factor subunit 1 isoform 1 [Homo sapiens]	1.93	1.30	1.64	1.82	1.27
ribosomal protein S6 kinase alpha-3 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
Na(+)/H(+) exchange regulatory cofactor NHE-RF1 [Homo sapiens]	0.75	0.69	2.35	1.63	2.39
U1 small nuclear ribonucleoprotein A [Homo sapiens]	0.83	1.51	0.99	0.94	0.90
small nuclear ribonucleoprotein Sm D2 isoform 1 [Homo sapiens]	1.96	1.31	1.87	0.40	0.76
tubulin-specific chaperone A isoform 2 [Homo sapiens]	3.21	0.94	0.88	2.01	0.84
programmed cell death protein 5 [Homo sapiens]	2.02	0.96	0.94	0.95	0.94
COP9 signalosome complex subunit 2 isoform 1 [Homo sapiens]	5.66	0.92	1.37	1.59	1.17
translin isoform 1 [Homo sapiens]	2.02	1.90	1.71	1.74	1.35
annexin A7 isoform 2 [Homo sapiens]	5.87	1.44	1.34	1.00	1.25
annexin A3 [Homo sapiens]	0.75	2.01	2.00	2.76	1.94
F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	0.62	1.30	1.30	1.56	1.74
copper chaperone for superoxide dismutase [Homo sapiens]	15.43	1.44	0.95	0.54	1.25
ATP-dependent RNA helicase DDX1 [Homo sapiens]		5.11	7.98	6.33	5.67
haptoglobin isoform 1 preproprotein [Homo sapiens]	0.57	5.03	3.07	1.75	4.50
insulin-like growth factor-binding protein complex acid labile subunit isoform 2 precursor [Homo sapiens]	0.62	0.54	0.25	0.13	0.27
serine/threonine-protein kinase OSR1 [Homo sapiens]	3.39	0.97	2.26	0.75	0.88
profilin-1 [Homo sapiens]	0.77	1.26	1.50	1.70	1.30
serpin B10 [Homo sapiens]	0.67	1.44	1.52	1.58	1.23
lysosomal Pro-X carboxypeptidase isoform 1 preproprotein [Homo sapiens]	2.54	1.17	1.26	0.73	0.94

cAMP-dependent protein kinase catalytic subunit PRKX [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
glutamine--tRNA ligase isoform a [Homo sapiens]	10.98	1.34	0.69	0.45	0.95
ras-related C3 botulinum toxin substrate 3 [Homo sapiens]	0.35	0.91	0.85	1.25	0.91
UV excision repair protein RAD23 homolog A isoform 1 [Homo sapiens]	1.34	0.78	0.40	0.21	0.57
RNA-binding protein 8A [Homo sapiens]	1.00	0.88	0.65	0.63	0.81
peptidoglycan recognition protein 1 precursor [Homo sapiens]	0.83	1.25	0.90	0.93	1.48
ubiquitin carboxyl-terminal hydrolase 14 isoform a [Homo sapiens]	19.15	0.91	1.58	1.96	1.18
actin, alpha cardiac muscle 1 proprotein [Homo sapiens]	2.79	0.94	0.49	0.31	0.69
carbonic anhydrase 3 [Homo sapiens]	54.82	0.79	0.98	0.26	0.75
calmodulin-like protein 3 [Homo sapiens]	1.44	1.22	2.35	1.38	1.79
crk-like protein [Homo sapiens]	2.66	1.25	1.59	1.72	1.33
cystatin-A [Homo sapiens]	0.69	1.30	1.62	1.47	2.31
neutrophil defensin 3 preproprotein [Homo sapiens]	0.54	2.49	1.41	2.17	2.24
RNA-binding protein EWS isoform 2 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 precursor [Homo sapiens]	0.57	1.41	1.89	0.98	1.27
histone H1.0 [Homo sapiens]	0.33	1.19	1.54	2.47	1.23
histone H1.2 [Homo sapiens]	0.46	2.10	2.56	2.67	6.31
histone H1.3 [Homo sapiens]	0.28	1.39	1.93	3.43	5.49
histone H1.4 [Homo sapiens]	0.35	1.95	2.20	7.54	6.54
histone H1.5 [Homo sapiens]	0.39	1.44	1.26	1.76	1.88
histone H3.3 [Homo sapiens]	0.43	2.29	0.57	0.31	2.30
hemoglobin subunit theta-1 [Homo sapiens]	2.66	0.98	0.58	0.37	0.96
hemoglobin subunit zeta [Homo sapiens]	126.77	2.45	1.54	0.32	0.96
structural maintenance of chromosomes protein 3 [Homo sapiens]	0.91	1.62	1.39	2.24	1.88
ubiquitin-conjugating enzyme E2 K isoform 1 [Homo sapiens]	4.99	0.98	2.56	2.05	2.45
rho-associated protein kinase 1 [Homo sapiens]	0.77	0.93	0.95	0.78	0.88
target of Myb protein 1 isoform 1 [Homo sapiens]	0.88	2.08	0.76	0.78	0.89
alpha-centractin [Homo sapiens]	2.15	2.59	1.51	1.40	1.24
actin-related protein 2 isoform b [Homo sapiens]	0.75	1.00	2.16	0.80	0.90
actin-related protein 3 isoform 1 [Homo sapiens]	1.64	2.71	1.34	1.40	2.30
actin-related protein 2/3 complex subunit 5 isoform 1 [Homo sapiens]	0.75	1.40	1.46	1.82	1.21
actin-related protein 2/3 complex subunit 4 isoform a [Homo sapiens]	0.77	2.71	1.87	1.89	2.34
actin-related protein 2/3 complex subunit 2 [Homo sapiens]	0.80	1.21	1.63	1.64	1.20
cofilin-1 [Homo sapiens]	0.80	1.19	1.62	2.06	1.45
complement factor H-related protein 2 precursor [Homo sapiens]	0.64	2.32	0.74	0.27	0.70
eukaryotic translation initiation factor 1b [Homo sapiens]	1.47	0.79	0.71	0.52	0.83
collagen type IV alpha-3-binding protein isoform 1 [Homo sapiens]	0.75	1.00	0.91	0.92	0.84
non-histone chromosomal protein HMG-17 [Homo sapiens]	0.19	1.41	2.16	4.81	1.90
heterogeneous nuclear ribonucleoprotein R isoform 2 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
inositol monophosphatase 1 isoform 1 [Homo sapiens]	1.18	1.21	1.60	1.51	1.57
lysine--tRNA ligase isoform 2 [Homo sapiens]	0.56	0.82	0.56	0.51	0.67

lymphocyte cytosolic protein 2 [Homo sapiens]	0.91	1.35	0.77	0.85	0.82
L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]	0.88	1.35	2.05	2.13	1.87
galectin-3-binding protein precursor [Homo sapiens]	1.18	1.21	0.78	0.51	1.70
lamin-B1 isoform 1 [Homo sapiens]	0.56	1.90	1.23	1.64	1.29
nitrilase homolog 1 isoform 1 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
protein disulfide-isomerase A6 isoform d precursor [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
nicotinamide phosphoribosyltransferase precursor [Homo sapiens]	0.88	1.82	2.21	2.57	1.56
26S proteasome non-ATPase regulatory subunit 14 [Homo sapiens]	1.44	0.94	0.70	0.61	0.84
glycogen phosphorylase, muscle form isoform 1 [Homo sapiens]	1.68	0.79	1.36	0.92	2.30
histone-binding protein RBBP4 isoform a [Homo sapiens]	0.52	2.20	1.22	0.85	0.88
protein S100-A11 [Homo sapiens]	0.80	1.88	2.81	4.59	2.66
protein S100-A12 [Homo sapiens]	0.64	1.87	2.47	1.74	2.47
eukaryotic translation initiation factor 1 [Homo sapiens]	1.47	0.79	0.71	0.52	0.83
CD5 antigen-like precursor [Homo sapiens]	0.46	0.97	0.40	0.23	0.65
guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens]	2.08	1.41	2.18	1.70	1.57
histone H1x [Homo sapiens]	0.21	1.96	0.79	1.80	1.61
S-adenosylmethionine synthase isoform type-2 [Homo sapiens]	1.96	0.95	0.55	0.46	0.81
malate dehydrogenase, cytoplasmic isoform 2 [Homo sapiens]	3.47	1.22	1.62	0.55	1.31
nucleosome assembly protein 1-like 4 [Homo sapiens]	7.52	1.44	1.54	2.01	1.30
reticulon-3 isoform a [Homo sapiens]	0.67	0.80	0.54	0.57	0.62
protein S100-A2 [Homo sapiens]	0.69	0.87	4.37	0.57	6.30
protein S100-P [Homo sapiens]	0.56	1.34	1.44	1.29	1.44
translin-associated protein X [Homo sapiens]	2.27	1.90	1.60	0.88	1.61
tubulin beta-4B chain [Homo sapiens]	0.98	0.66	1.42	0.69	1.42
ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 2 [Homo sapiens]	1.64	0.69	0.46	0.44	0.67
ribonuclease T2 precursor [Homo sapiens]	0.95	2.09	2.38	2.16	1.94
multifunctional protein ADE2 isoform 2 [Homo sapiens]	3.12	1.96	1.59	1.96	1.46
noelin isoform 2 precursor [Homo sapiens]	0.31	0.91	0.39	0.20	0.56
peroxiredoxin-4 precursor [Homo sapiens]	19.15	0.83	1.43	0.94	1.42
GTP-binding nuclear protein Ran isoform 1 [Homo sapiens]	4.79	2.08	1.24	0.89	1.17
craniofacial development protein 1 [Homo sapiens]	0.18	0.58	1.46	2.13	0.91
adenylyl cyclase-associated protein 2 [Homo sapiens]	0.77	1.28	2.11	2.55	1.52
adenylyl cyclase-associated protein 1 [Homo sapiens]	0.67	1.25	1.79	1.83	1.38
F-actin-capping protein subunit alpha-1 [Homo sapiens]	0.66	1.00	0.95	2.51	0.91
F-actin-capping protein subunit alpha-2 [Homo sapiens]	2.79	0.87	0.99	1.21	1.17
T-complex protein 1 subunit beta isoform 1 [Homo sapiens]	2.38	2.08	0.77	0.94	0.96
T-complex protein 1 subunit eta isoform a [Homo sapiens]	2.19	1.25	1.54	1.19	0.93
dynactin subunit 2 isoform 1 [Homo sapiens]	2.66	0.94	0.94	0.85	0.87
ubiquitin-like modifier-activating enzyme ATG7 isoform a [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
epididymal secretory protein E1 precursor [Homo sapiens]	0.41	3.52	2.49	3.23	1.86

dnaJ homolog subfamily B member 1 [Homo sapiens]	3.75	0.83	1.62	1.43	1.26
LIM and SH3 domain protein 1 isoform a [Homo sapiens]	0.64	0.64	0.77	0.71	0.80
acyl-protein thioesterase 1 isoform 1 [Homo sapiens]	0.80	0.79	0.82	0.99	0.90
myosin regulatory light chain 12A [Homo sapiens]	0.91	0.87	1.60	1.19	0.98
NEDD8 precursor [Homo sapiens]	1.82	1.62	1.39	2.38	1.27
acidic leucine-rich nuclear phosphoprotein 32 family member A [Homo sapiens]	0.88	1.53	1.80	1.60	1.45
phosphatidylinositol transfer protein alpha isoform [Homo sapiens]	1.51	0.94	0.89	0.68	0.96
phospholipid transfer protein isoform a precursor [Homo sapiens]	1.61	1.97	0.66	0.46	0.80
protein phosphatase 1 regulatory subunit 3D [Homo sapiens]	0.26	1.79	4.92	4.16	1.56
proteasome activator complex subunit 1 isoform 1 [Homo sapiens]	1.68	0.89	1.90	1.23	1.29
2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 1 [Homo sapiens]	1.18	0.96	0.46	0.24	0.67
semaphorin-3C precursor [Homo sapiens]	0.31	0.56	0.21	0.09	0.32
14-3-3 protein sigma [Homo sapiens]	2.79	0.42	2.18	0.24	2.67
acidic leucine-rich nuclear phosphoprotein 32 family member B [Homo sapiens]	1.31	1.45	1.58	1.19	2.53
serine/threonine-protein kinase 4 [Homo sapiens]	0.75	0.66	0.56	0.74	0.67
transforming acidic coiled-coil-containing protein 3 [Homo sapiens]	0.28	0.93	1.21	2.77	0.84
valine--tRNA ligase [Homo sapiens]	0.77	0.68	0.58	0.44	0.69
dual specificity mitogen-activated protein kinase kinase 1 [Homo sapiens]	2.19	0.77	2.29	1.34	1.88
apoptosis inhibitor 5 isoform b [Homo sapiens]	0.50	0.85	0.70	0.69	0.79
tripeptidyl-peptidase 1 preproprotein [Homo sapiens]	0.98	2.08	0.79	1.44	1.74
COP9 signalosome complex subunit 8 isoform 1 [Homo sapiens]	2.11	2.08	0.71	0.51	0.66
diphosphoinositol polyphosphate phosphohydrolase 1 [Homo sapiens]	0.57	0.93	1.51	1.78	1.74
guanine nucleotide-binding protein G(k) subunit alpha [Homo sapiens]	0.57	0.97	0.82	0.64	0.84
heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]	1.82	1.26	1.29	1.18	1.61
26S protease regulatory subunit 6B isoform 1 [Homo sapiens]	4.40	1.25	1.00	0.66	0.75
ras-related GTP-binding protein A [Homo sapiens]	1.24	0.91	0.46	0.35	0.67
KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 1 [Homo sapiens]	0.77	0.96	1.81	2.29	1.37
fibroleukin precursor [Homo sapiens]	2.70	2.66	1.39	2.14	2.80
destrin isoform a [Homo sapiens]	0.31	0.79	0.95	1.41	2.60
thioredoxin-dependent peroxide reductase, mitochondrial isoform a precursor [Homo sapiens]	1.47	1.45	1.82	2.30	1.81
protein diaphanous homolog 2 isoform 156 [Homo sapiens]	0.21	1.17	1.93	3.09	1.20
gamma-enolase [Homo sapiens]	0.77	1.90	0.88	0.73	0.90
endoplasmic reticulum resident protein 29 isoform 1 precursor [Homo sapiens]	0.83	1.38	2.00	1.64	1.25
stress-induced-phosphoprotein 1 isoform b [Homo sapiens]	4.26	0.95	1.46	2.05	1.47
transaldolase [Homo sapiens]	1.64	1.29	1.71	2.29	1.57
14-3-3 protein epsilon [Homo sapiens]	3.79	2.59	2.01	2.07	1.17
14-3-3 protein theta [Homo sapiens]	1.51	1.30	1.21	0.80	0.82
hsp90 co-chaperone Cdc37 [Homo sapiens]	1.28	0.80	1.62	2.07	0.84
cleavage and polyadenylation specificity factor subunit	1.31	1.62	0.61	0.39	0.68

5 [Homo sapiens]

folistatin-related protein 1 precursor [Homo sapiens]	0.64	6.43	0.76	0.38	1.29
U6 snRNA-associated Sm-like protein LSm6 [Homo sapiens]	4.89	2.32	1.34	1.34	1.21
reticulon-4 isoform C [Homo sapiens]	7.95	1.51	1.30	1.96	0.90
serpin B3 [Homo sapiens]	4.65	0.99	2.75	0.61	7.46
serine/arginine-rich splicing factor 1 isoform 1 [Homo sapiens]	0.69	1.24	0.66	0.29	0.82
solute carrier family 2, facilitated glucose transporter member 3 [Homo sapiens]	0.52	1.62	1.74	0.71	0.64
small nuclear ribonucleoprotein Sm D1 isoform 1 [Homo sapiens]	0.77	1.47	1.43	1.93	1.35
spectrin beta chain, non-erythrocytic 2 [Homo sapiens]	3.26	1.40	2.19	2.76	1.17
gamma-aminobutyric acid receptor-associated protein [Homo sapiens]	1.57	1.27	1.64	1.60	1.44
proline synthase co-transcribed bacterial homolog protein [Homo sapiens]	3.56	1.47	2.49	4.11	1.71
twinfilin-2 [Homo sapiens]	1.31	0.98	1.26	1.41	2.76
transcription elongation factor B polypeptide 2 isoform a [Homo sapiens]	1.47	1.21	1.27	1.52	1.81
splicing factor U2AF 65 kDa subunit isoform a [Homo sapiens]	1.71	1.40	2.56	1.89	1.20
transitional endoplasmic reticulum ATPase [Homo sapiens]	6.09	1.73	1.43	1.65	2.68
clathrin light chain A isoform b [Homo sapiens]	1.47	0.76	0.79	2.51	0.75
glutathione peroxidase 3 precursor [Homo sapiens]	0.75	1.40	0.49	0.27	0.74
protein diaphanous homolog 2 isoform 12C [Homo sapiens]	0.21	1.17	1.93	3.09	1.20
rab GDP dissociation inhibitor beta isoform 1 [Homo sapiens]	3.26	1.36	1.74	1.52	1.62
serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 1 [Homo sapiens]	0.57	1.73	1.29	0.98	0.71
hemoglobin subunit gamma-2 [Homo sapiens]	65.65	0.77	0.76	0.27	0.95
alpha-synuclein isoform NACP112 [Homo sapiens]	63.90	0.91	0.81	0.33	0.84
peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	1.34	0.91	1.18	1.46	2.45
DCC-interacting protein 13-alpha [Homo sapiens]	4.12	1.44	1.40	1.31	0.92
activator of 90 kDa heat shock protein ATPase homolog 1 [Homo sapiens]	0.88	0.77	0.62	0.58	0.63
echinoderm microtubule-associated protein-like 2 isoform 2 [Homo sapiens]	0.56	1.34	0.69	0.69	1.23
grancalcin [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
glyoxylate reductase/hydroxypyruvate reductase [Homo sapiens]	0.75	0.94	0.68	0.69	0.92
microtubule-associated protein RP/EB family member 1 [Homo sapiens]	1.28	0.92	0.95	1.17	0.81
mitochondrial peptide methionine sulfoxide reductase isoform a precursor [Homo sapiens]	0.80	1.73	2.68	1.41	0.96
6-phosphogluconolactonase [Homo sapiens]	1.71	0.94	0.90	0.98	1.82
phosphatidylinositol transfer protein beta isoform isoform 1 [Homo sapiens]	1.31	1.51	0.99	0.75	0.89
acidic leucine-rich nuclear phosphoprotein 32 family member C [Homo sapiens]	2.27	1.28	2.54	3.82	2.06
histone H2A.V isoform 1 [Homo sapiens]	0.41	3.48	0.91	1.26	1.28
glutaminy-peptide cyclotransferase precursor [Homo sapiens]	0.75	1.96	0.61	0.54	0.75
ras suppressor protein 1 isoform 1 [Homo sapiens]	1.76	2.59	1.54	0.98	1.54
transportin-3 isoform 1 [Homo sapiens]	4.55	0.70	0.35	0.45	0.38
choline/ethanolamine kinase [Homo sapiens]	0.23	1.90	1.43	1.72	1.20
histidine--tRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26

cytochrome b-245 heavy chain [Homo sapiens]	0.95	1.25	1.37	0.95	1.74
proSAAS preproprotein [Homo sapiens]	2.66	2.18	1.27	1.38	1.72
vacuolar protein sorting-associated protein 4A [Homo sapiens]	1.24	0.83	1.21	2.02	1.23
apoptotic protease-activating factor 1 isoform a [Homo sapiens]	0.77	0.85	1.68	1.37	1.29
proto-oncogene vav isoform 1 [Homo sapiens]	0.75	0.88	0.56	0.52	0.78
adenylate kinase 2, mitochondrial isoform b [Homo sapiens]	1.18	1.18	1.39	1.23	1.17
calcyclin-binding protein isoform 1 [Homo sapiens]	1.34	1.39	2.73	3.92	1.83
coronin-1C isoform b [Homo sapiens]	0.66	0.98	1.31	1.75	2.76
copine-7 isoform b [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
tRNA-splicing ligase RtcB homolog [Homo sapiens]	1.21	0.93	1.18	1.47	2.08
EH domain-containing protein 3 [Homo sapiens]	3.21	0.94	0.78	0.75	0.90
ERO1-like protein alpha precursor [Homo sapiens]	0.41	1.42	2.09	1.47	1.43
protein canopy homolog 2 isoform 1 precursor [Homo sapiens]	7.48	1.30	1.75	1.35	2.53
inositol monophosphatase 2 [Homo sapiens]	6.48	0.71	0.69	0.55	0.71
sister chromatid cohesion protein PDS5 homolog B [Homo sapiens]	0.14	1.88	3.83	7.23	4.01
U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens]	0.75	1.21	0.95	0.67	0.98
28 kDa heat- and acid-stable phosphoprotein [Homo sapiens]	0.62	1.18	1.45	2.24	1.61
protein S100-A6 [Homo sapiens]	3.75	1.46	2.31	3.61	3.57
sorting nexin-5 isoform a [Homo sapiens]	0.33	0.77	0.96	1.28	2.30
heme-binding protein 2 [Homo sapiens]	1.21	1.62	1.27	1.27	2.08
ras-related protein Rap-1b isoform 1 precursor [Homo sapiens]	0.98	1.39	1.87	2.08	1.45
regulator complex protein LAMTOR2 isoform 1 [Homo sapiens]	1.64	1.44	1.44	1.24	2.60
m7GpppX diphosphatase [Homo sapiens]	0.75	2.08	0.94	0.88	0.85
protein phosphatase 1F [Homo sapiens]	4.65	1.45	2.29	1.33	1.79
arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 [Homo sapiens]	5.93	2.71	0.82	0.67	1.23
rho GTPase-activating protein 25 isoform b [Homo sapiens]	0.64	1.00	1.43	0.98	0.94
26S proteasome non-ATPase regulatory subunit 6 isoform 2 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
eukaryotic initiation factor 4A-III [Homo sapiens]	0.45	0.88	0.56	0.79	0.74
ras-related protein Rab-21 [Homo sapiens]	1.34	1.94	2.10	3.47	1.75
clathrin interactor 1 isoform 2 [Homo sapiens]	0.39	0.97	1.93	1.48	1.30
glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]	1.64	1.27	1.87	1.30	1.59
lysosome-associated membrane glycoprotein 2 isoform B precursor [Homo sapiens]	0.83	1.77	1.61	0.92	1.88
vinculin isoform meta-VCL [Homo sapiens]	0.88	1.96	1.27	1.29	1.30
actin-like protein 6B [Homo sapiens]	0.45	2.07	3.60	3.63	1.81
ubiquitin-fold modifier 1 isoform 1 precursor [Homo sapiens]	1.31	0.63	0.61	0.58	0.67
translation machinery-associated protein 7 [Homo sapiens]	0.62	1.27	2.45	5.81	1.60
EKC/KEOPS complex subunit TPRKB [Homo sapiens]	20.02	1.30	1.24	2.77	1.00
complement C1q subcomponent subunit A precursor [Homo sapiens]	0.75	2.45	0.66	0.33	0.73
hematological and neurological expressed 1 protein isoform 1 [Homo sapiens]	0.39	0.82	1.72	2.27	0.53
protein Z-dependent protease inhibitor precursor [Homo sapiens]	0.66	0.98	0.65	0.32	0.70

protein CutA isoform 2 precursor [Homo sapiens]	1.44	1.18	0.88	0.82	0.89
U6 snRNA-associated Sm-like protein LSm7 [Homo sapiens]	1.31	1.24	1.41	1.53	1.18
LSM8 homolog, U6 small nuclear RNA associated [Homo sapiens]	4.26	0.94	0.41	0.30	0.62
vacuolar protein sorting-associated protein 29 isoform 1 [Homo sapiens]	0.77	1.73	1.44	1.45	2.68
dnaJ homolog subfamily B member 11 precursor [Homo sapiens]	2.08	2.74	1.31	0.83	1.41
UMP-CMP kinase isoform a [Homo sapiens]	3.21	0.78	0.88	1.43	0.66
ras-related protein Rab-8B [Homo sapiens]	0.62	0.64	0.56	0.49	0.78
protachykinin-1 isoform gamma precursor [Homo sapiens]		0.75	0.34	0.15	0.38
ficolin-1 precursor [Homo sapiens]	0.66	1.90	2.18	2.26	1.64
ficolin-2 isoform b precursor [Homo sapiens]	0.45	1.18	0.93	0.49	1.45
RNA-binding protein Raly isoform 1 [Homo sapiens]	0.54	0.94	0.98	0.98	0.90
protein mago nashi homolog 2 isoform 1 [Homo sapiens]	2.34	1.59	2.33	3.87	1.61
septin-11 [Homo sapiens]	1.24	0.92	1.34	1.18	1.74
GTPase IMAP family member 4 [Homo sapiens]	0.62	0.57	0.55	0.63	0.67
mycophenolic acid acyl-glucuronide esterase, mitochondrial isoform 1 precursor [Homo sapiens]	2.38	1.90	2.10	1.54	1.94
leucine-rich repeat flightless-interacting protein 2 isoform 2 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
nicotinamide riboside kinase 1 isoform 1 [Homo sapiens]	4.50	1.51	0.77	0.82	0.88
regulator complex protein LAMTOR1 [Homo sapiens]	2.54	0.94	0.58	0.51	0.89
WD repeat-containing protein 1 isoform 1 [Homo sapiens]	1.31	1.30	1.30	0.96	1.37
SAM and SH3 domain-containing protein 3 [Homo sapiens]	1.37	0.63	0.50	0.50	0.63
heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]	4.84	1.69	2.26	3.89	1.47
40S ribosomal protein SA [Homo sapiens]	1.71	1.44	1.38	2.46	1.50
ras-related C3 botulinum toxin substrate 1 isoform Rac1b [Homo sapiens]	0.39	0.91	1.44	2.32	1.18
ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sapiens]	0.39	0.91	1.44	2.32	1.18
phosphoribosyltransferase domain-containing protein 1 isoform 1 [Homo sapiens]	10.14	1.28	1.62	1.42	1.88
UDP-glucose:glycoprotein glucosyltransferase 1 precursor [Homo sapiens]	0.95	1.29	1.26	1.30	0.85
omega-amidase NIT2 [Homo sapiens]	5.72	0.92	0.94	0.82	0.83
adenosylhomocysteinase isoform 1 [Homo sapiens]	3.90	0.95	1.62	1.56	2.30
acyl-protein thioesterase 2 [Homo sapiens]	0.54	0.96	0.63	0.73	1.61
resistin precursor [Homo sapiens]	1.71	1.90	1.57	1.61	1.26
PEST proteolytic signal-containing nuclear protein [Homo sapiens]	1.54	0.77	1.82	2.30	0.65
fructose-2,6-bisphosphatase TIGAR [Homo sapiens]	2.54	1.96	1.74	1.60	1.26
eukaryotic translation initiation factor 5A-2 [Homo sapiens]	16.01	0.68	1.44	2.02	1.35
actin-related protein 3B isoform 1 [Homo sapiens]	1.24	1.26	1.77	2.19	1.37
pyridoxal phosphate phosphatase [Homo sapiens]	38.25	1.53	2.44	1.87	2.35
calnexin precursor [Homo sapiens]	0.64	1.45	1.62	1.38	1.23
histone H2A type 1-D [Homo sapiens]	1.41	1.77	0.53	0.24	0.79
histone H2B type 1-B [Homo sapiens]	0.57	15.16	1.27	0.29	4.54
histone cluster 1, H2aj [Homo sapiens]	1.41	1.77	0.53	0.24	0.79
microtubule-associated protein RP/EB family member 3 [Homo sapiens]	1.71	0.96	1.42	1.93	1.26
interleukin-8 precursor [Homo sapiens]	1.28	13.87	4.73	2.49	17.73

transforming protein RhoA precursor [Homo sapiens]	1.18	0.94	1.26	1.63	2.60
cysteine--tRNA ligase, cytoplasmic isoform b [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
N-alpha-acetyltransferase 10 isoform 1 [Homo sapiens]	0.52	1.73	6.21	9.21	2.53
nucleophosmin isoform 1 [Homo sapiens]	0.67	1.51	1.94	1.64	1.52
pyruvate kinase PKLR isoform 1 [Homo sapiens]	0.43	0.87	1.78	1.72	1.27
high mobility group nucleosome-binding domain-containing protein 4 [Homo sapiens]	1.37	2.45	0.76	1.52	2.60
apoptosis-associated speck-like protein containing a CARD isoform a [Homo sapiens]	2.38	1.26	1.87	2.44	1.81
thymosin beta-10 [Homo sapiens]	0.57	0.92	1.36	1.24	0.77
MAP kinase-activated protein kinase 2 isoform 1 [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
E3 ubiquitin-protein ligase TRIP12 isoform c [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	3.12	1.62	1.87	2.30	1.80
X-ray repair cross-complementing protein 5 [Homo sapiens]	0.80	0.97	1.30	1.26	1.94
phosphoserine aminotransferase isoform 2 [Homo sapiens]	2.46	0.84	0.89	1.20	1.20
U6 snRNA-associated Sm-like protein LSm2 [Homo sapiens]	2.58	0.81	0.67	0.30	0.84
lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	0.28	0.81	0.64	0.91	0.88
ras-related protein Rab-18 isoform 1 [Homo sapiens]	0.69	0.92	0.83	2.21	0.74
ATP-binding cassette sub-family F member 1 isoform b [Homo sapiens]	2.79	2.59	0.89	0.75	0.92
arginase-1 isoform 2 [Homo sapiens]	2.79	1.00	0.92	1.77	1.45
serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform b [Homo sapiens]	0.77	0.82	0.62	0.55	0.68
tubulin--tyrosine ligase-like protein 12 [Homo sapiens]	1.54	0.80	0.91	1.37	0.85
inorganic pyrophosphatase [Homo sapiens]	4.65	1.18	2.12	2.74	1.71
thymosin beta-4 [Homo sapiens]	0.28	0.82	2.12	3.65	0.83
cytochrome c [Homo sapiens]	4.99	1.70	5.90	1.76	3.69
72 kDa type IV collagenase isoform a preproprotein [Homo sapiens]	1.51	4.10	0.89	0.56	0.82
azurocidin preproprotein [Homo sapiens]	0.69	2.50	0.84	0.98	0.93
beta-centractin [Homo sapiens]	1.64	1.39	1.83	2.41	1.26
prosaposin isoform a preproprotein [Homo sapiens]	0.95	2.74	2.19	1.95	1.98
cytidine deaminase [Homo sapiens]	0.56	0.87	0.84	1.20	1.82
wiskott-Aldrich syndrome protein family member 2 isoform 1 [Homo sapiens]	0.91	0.85	2.76	0.62	1.22
regulator complex protein LAMTOR3 isoform 1 [Homo sapiens]	5.93	3.82	6.46	6.72	3.39
Golgi phosphoprotein 3 [Homo sapiens]	0.98	1.76	4.34	5.63	2.53
gamma-parvin [Homo sapiens]	2.00	0.64	0.62	1.43	0.66
eukaryotic translation initiation factor 4H isoform 1 [Homo sapiens]	1.44	0.82	0.91	1.43	0.96
coatamer subunit gamma-1 [Homo sapiens]	1.51	1.44	2.33	3.74	1.69
Golgi-associated plant pathogenesis-related protein 1 isoform a [Homo sapiens]	0.66	0.91	1.78	2.55	1.94
mannose-1-phosphate guanyltransferase beta isoform 1 [Homo sapiens]	7.05	0.96	0.96	0.88	0.92
mannose-1-phosphate guanyltransferase beta isoform 2 [Homo sapiens]	7.05	0.96	0.96	0.88	0.92
fibrinogen alpha chain isoform alpha preproprotein [Homo sapiens]	1.41	1.76	1.46	0.96	2.13
coatamer subunit delta isoform 1 [Homo sapiens]	0.33	2.59	1.93	2.25	1.50
40S ribosomal protein S18 [Homo sapiens]	3.56	1.25	1.18	1.43	2.59

alpha-actinin-4 [Homo sapiens]	0.77	2.08	1.46	1.66	1.23
rRNA 2'-O-methyltransferase fibrillarin [Homo sapiens]	0.77	0.85	0.31	0.15	0.50
sialic acid synthase [Homo sapiens]	1.82	0.98	1.96	1.47	1.24
COP9 signalosome complex subunit 7b isoform b [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
calpain-1 catalytic subunit [Homo sapiens]	4.16	0.91	1.19	1.39	0.97
myosin-9 [Homo sapiens]	0.83	2.08	1.42	1.88	1.18
glucosamine-6-phosphate isomerase 1 [Homo sapiens]	1.79	0.87	0.78	0.51	0.81
DDRCK domain-containing protein 1 precursor [Homo sapiens]		3.52	4.19	9.42	1.61
small nuclear ribonucleoprotein-associated protein N [Homo sapiens]	2.79	2.82	5.60	7.21	2.69
myosin-11 isoform SM2A [Homo sapiens]	0.98	1.19	1.64	2.01	1.51
myosin-11 isoform SM1A [Homo sapiens]	0.98	1.19	1.64	2.01	1.51
histone deacetylase 1 [Homo sapiens]	0.25	1.29	1.59	2.77	1.27
uncharacterized protein C19orf43 [Homo sapiens]		0.93	0.82	0.81	0.62
gamma-glutamylcyclotransferase isoform 1 [Homo sapiens]	4.99	1.34	1.41	1.34	1.78
dynactin subunit 1 isoform 2 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
dynactin subunit 1 isoform 1 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
sulfhydryl oxidase 1 isoform a precursor [Homo sapiens]	1.31	1.89	0.84	0.97	1.37
UPF0364 protein C6orf211 isoform a [Homo sapiens]	1.21	0.83	1.27	1.75	1.88
WD repeat-containing protein 61 [Homo sapiens]	2.46	1.21	1.54	1.56	0.94
immunoglobulin lambda-like polypeptide 1 isoform a precursor [Homo sapiens]	0.39	0.87	0.37	0.18	0.53
dual specificity mitogen-activated protein kinase kinase 2 [Homo sapiens]	1.24	0.77	0.75	1.00	2.08
probable ATP-dependent RNA helicase DDX4 isoform 1 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
complement factor H-related protein 5 precursor [Homo sapiens]	0.66	1.62	2.07	0.44	0.91
acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 1 [Homo sapiens]	0.95	0.80	0.83	1.97	0.90
ras-related protein Rab-1B [Homo sapiens]	0.80	1.28	1.39	2.25	1.48
DNA-dependent protein kinase catalytic subunit isoform 1 [Homo sapiens]	1.41	0.94	0.80	1.00	0.97
heat shock-related 70 kDa protein 2 [Homo sapiens]	0.83	1.30	0.66	0.38	0.82
wiskott-Aldrich syndrome protein family member 3 isoform 1 [Homo sapiens]	0.80	0.85	2.76	0.42	1.22
SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]	1.18	1.42	1.91	1.80	1.71
tryptase alpha/beta-1 precursor [Homo sapiens]	1.31	0.62	0.37	0.40	0.43
gamma-aminobutyric acid receptor-associated protein-like 1 [Homo sapiens]	1.57	1.47	1.54	1.00	1.20
40S ribosomal protein S5 [Homo sapiens]	1.68	0.94	0.78	0.81	0.68
SH3 domain-containing kinase-binding protein 1 isoform a [Homo sapiens]	2.00	1.25	1.48	2.06	1.28
heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapiens]	0.50	1.00	1.83	2.47	1.21
heterogeneous nuclear ribonucleoprotein D0 isoform b [Homo sapiens]	0.50	0.96	1.29	2.11	1.28
heterogeneous nuclear ribonucleoprotein D0 isoform a [Homo sapiens]	0.50	1.00	1.83	2.47	1.21
heterogeneous nuclear ribonucleoprotein M isoform a [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
heterogeneous nuclear ribonucleoprotein H3 isoform b [Homo sapiens]	0.91	0.85	0.84	1.39	0.84
heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]	0.88	0.81	1.39	1.82	1.42
poly(rC)-binding protein 2 isoform b [Homo sapiens]	1.64	0.82	2.47	5.20	1.96

poly(rC)-binding protein 2 isoform a [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
ubiquitin carboxyl-terminal hydrolase 15 isoform 2 [Homo sapiens]	6.25	1.00	0.95	1.40	0.82
coronin-1B [Homo sapiens]	0.45	0.78	1.54	0.98	1.29
partner of Y14 and mago isoform 1 [Homo sapiens]	0.80	1.87	0.93	1.81	1.46
protein Hook homolog 3 [Homo sapiens]	0.83	0.77	1.30	1.98	0.94
heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]	1.64	0.79	1.43	2.16	2.30
heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]	1.64	0.79	1.43	2.16	2.30
collagen type IV alpha-3-binding protein isoform 2 [Homo sapiens]	0.75	1.00	0.91	0.92	0.84
polypyrimidine tract-binding protein 1 isoform b [Homo sapiens]	1.57	1.51	1.58	1.91	1.45
polypyrimidine tract-binding protein 1 isoform c [Homo sapiens]	1.57	1.51	1.58	1.91	1.45
protein phosphatase 1 regulatory subunit 12B isoform c [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
alpha-internexin [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
thioredoxin domain-containing protein 17 [Homo sapiens]	1.89	1.39	1.83	1.96	1.64
alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens]	3.65	1.45	1.68	1.33	1.39
transcription elongation factor A protein-like 3 [Homo sapiens]	0.75	0.73	1.95	2.48	0.50
peptidyl-prolyl cis-trans isomerase-like 3 isoform PPIL3a [Homo sapiens]	3.34	0.97	1.43	1.98	0.95
protein FAM65B isoform 2 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
tubulin alpha-1C chain [Homo sapiens]	1.00	0.73	0.99	0.51	0.84
complement C2 isoform 1 preproprotein [Homo sapiens]	0.35	1.96	0.62	0.32	0.67
allograft inflammatory factor 1 isoform 3 [Homo sapiens]	0.77	0.98	1.31	1.23	2.39
dual specificity mitogen-activated protein kinase kinase 6 [Homo sapiens]	0.77	0.63	0.71	0.55	0.74
60S ribosomal protein L5 [Homo sapiens]	1.44	1.19	1.96	1.26	1.28
eukaryotic translation initiation factor 4H isoform 2 [Homo sapiens]	1.44	0.82	0.91	1.43	0.96
caspase-3 preproprotein [Homo sapiens]	1.44	0.88	0.85	0.96	0.88
mimecan preproprotein [Homo sapiens]	3.39	2.08	0.63	0.49	1.19
AP-2 complex subunit mu isoform a [Homo sapiens]	1.31	1.40	0.69	0.64	0.84
serine/threonine-protein kinase MST4 isoform 1 [Homo sapiens]	1.93	2.45	1.58	1.27	1.56
rho guanine nucleotide exchange factor 1 isoform 2 [Homo sapiens]	1.51	0.96	0.77	0.68	0.83
rho guanine nucleotide exchange factor 2 isoform 3 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
probable histidine--tRNA ligase, mitochondrial isoform 1 precursor [Homo sapiens]	4.55	1.00	1.26	1.44	2.76
serine/arginine-rich splicing factor 8 [Homo sapiens]	0.39	1.44	1.41	2.44	2.60
chromobox protein homolog 3 [Homo sapiens]	2.00	1.73	1.60	1.87	1.19
arginine--tRNA ligase, cytoplasmic [Homo sapiens]	2.33	0.79	0.70	0.56	0.80
60S ribosomal protein L11 isoform 1 [Homo sapiens]	1.47	1.47	1.38	1.73	1.54
protein PML isoform 9 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
protein PML isoform 10 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
caspase-4 isoform gamma precursor [Homo sapiens]	0.62	1.38	2.16	1.36	1.94
granzyme H isoform 1 precursor [Homo sapiens]	0.33	0.61	0.31	0.20	0.49
histidine protein methyltransferase 1 homolog [Homo sapiens]	0.45	1.73	0.54	0.31	0.64
hexokinase-2 [Homo sapiens]	4.74	1.62	1.31	1.25	1.17

histone H2A type 3 [Homo sapiens]	1.79	1.74	0.50	0.20	0.68
cAMP-dependent protein kinase catalytic subunit gamma [Homo sapiens]	0.52	0.71	0.55	0.60	0.66
arachidonate 5-lipoxygenase-activating protein isoform 1 [Homo sapiens]	7.95	0.93	0.55	0.41	0.62
TFIIH basal transcription factor complex helicase XPD subunit isoform 1 [Homo sapiens]	0.28	1.39	3.23	4.06	2.56
collagen alpha-5(IV) chain isoform 2 precursor [Homo sapiens]	1.28	0.76	0.56	0.69	0.76
hexokinase-1 isoform HKI-R [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
serine--tRNA ligase, cytoplasmic [Homo sapiens]	1.64	0.76	0.53	0.48	0.67
selenium-binding protein 1 isoform 1 [Homo sapiens]	2.31	0.82	0.67	0.35	0.81
histone H2B type 1-O [Homo sapiens]	0.57	15.16	1.27	0.29	4.54
cell division control protein 42 homolog isoform 2 [Homo sapiens]	2.00	1.62	2.16	2.25	1.35
testis-specific serine/threonine-protein kinase 3 [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	1.00	3.17	1.31	0.71	1.61
78 kDa glucose-regulated protein precursor [Homo sapiens]	0.98	1.44	1.74	1.34	1.24
60S ribosomal protein L4 [Homo sapiens]	0.69	1.45	3.20	3.19	1.93
caspase recruitment domain-containing protein 16 isoform 2 [Homo sapiens]	0.41	0.77	0.56	0.91	0.63
ubiquilin-1 isoform 1 [Homo sapiens]	1.28	1.24	0.91	0.87	1.20
ubiquilin-1 isoform 2 [Homo sapiens]	1.28	1.24	0.91	0.87	1.20
ubiquilin-2 [Homo sapiens]	1.28	1.24	0.91	0.87	1.20
src kinase-associated phosphoprotein 2 [Homo sapiens]	1.21	1.29	1.19	1.28	1.18
protein Niban [Homo sapiens]	0.64	0.77	1.18	1.53	0.82
fibronectin isoform 3 preproprotein [Homo sapiens]	0.69	1.42	0.70	0.74	1.38
60S acidic ribosomal protein P0 [Homo sapiens]	1.44	1.18	1.36	2.51	0.81
ras-related protein Rab-8A [Homo sapiens]	0.95	0.92	1.21	1.21	2.16
60S ribosomal protein L23a [Homo sapiens]	0.54	0.85	0.62	1.48	0.96
noelin isoform 1 precursor [Homo sapiens]	0.31	0.91	0.39	0.20	0.56
N-alpha-acetyltransferase 15, NatA auxiliary subunit [Homo sapiens]	1.18	1.40	0.80	0.76	0.71
ARF GTPase-activating protein GIT2 isoform 1 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
ARF GTPase-activating protein GIT2 isoform 2 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapiens]	1.28	2.08	0.96	1.93	1.18
40S ribosomal protein S6 [Homo sapiens]	0.41	0.92	2.16	1.74	1.00
phosphoserine aminotransferase isoform 1 [Homo sapiens]	2.46	0.84	0.89	1.20	1.20
far upstream element-binding protein 1 [Homo sapiens]	0.77	0.77	0.98	0.82	2.60
vacuolar protein sorting-associated protein 29 isoform 2 [Homo sapiens]	0.77	1.73	1.44	1.45	2.68
PREDICTED: nuclear transport factor 2-like [Homo sapiens]	29.69	1.26	2.28	2.52	2.02
vacuolar protein sorting-associated protein 4B [Homo sapiens]	1.82	0.83	2.69	1.53	1.61
vascular non-inflammatory molecule 2 isoform 1 precursor [Homo sapiens]	0.50	0.80	0.43	0.29	0.78
vascular non-inflammatory molecule 2 isoform 2 [Homo sapiens]	0.50	0.80	0.43	0.29	0.78
tubulin alpha-4A chain isoform 1 [Homo sapiens]	0.41	0.88	0.93	0.67	1.81
tubulin alpha-3C/D chain [Homo sapiens]	0.75	0.71	0.69	0.46	0.78

vacuolar protein sorting-associated protein 18 homolog [Homo sapiens]	0.06	0.78	1.58	3.34	1.74
myosin light polypeptide 6 isoform 1 [Homo sapiens]	0.77	0.93	1.28	1.59	2.39
vacuolar protein sorting-associated protein 35 [Homo sapiens]	1.31	0.85	0.66	0.62	0.70
dynein light chain 2, cytoplasmic [Homo sapiens]	0.50	0.71	0.38	0.22	0.46
tyrosine-protein phosphatase non-receptor type 6 isoform 1 [Homo sapiens]	0.50	0.77	0.88	1.26	0.76
tyrosine-protein phosphatase non-receptor type 6 isoform 2 [Homo sapiens]	0.50	0.77	0.88	1.26	0.76
tyrosine-protein phosphatase non-receptor type 6 isoform 3 [Homo sapiens]	0.52	0.75	0.85	0.97	0.76
histone H2A type 1-H [Homo sapiens]	1.41	1.77	0.53	0.24	0.79
histone H2B type 1-K [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens]	0.98	0.97	2.49	1.92	1.81
synaptic vesicle membrane protein VAT-1 homolog [Homo sapiens]	1.64	1.00	0.80	0.77	0.85
dr1-associated corepressor [Homo sapiens]	0.77	1.62	0.97	0.98	0.93
dipeptidyl peptidase 3 isoform 1 [Homo sapiens]	1.37	0.91	0.58	0.43	0.70
26S proteasome non-ATPase regulatory subunit 9 isoform 1 [Homo sapiens]	3.90	0.69	0.52	0.61	0.62
beta-catenin-like protein 1 isoform 1 [Homo sapiens]	7.48	2.29	2.24	4.58	2.50
MOB kinase activator 3A [Homo sapiens]	0.62	1.28	0.69	0.50	0.91
copine-4 isoform 2 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
dynein heavy chain 5, axonemal [Homo sapiens]	3.12	2.45	0.70	0.43	0.79
cullin-2 isoform c [Homo sapiens]	2.34	0.79	0.95	0.99	0.94
ubiquitin-like-conjugating enzyme ATG3 isoform 1 [Homo sapiens]	2.76	0.88	1.56	4.80	1.31
histone H2A type 1-B/E [Homo sapiens]	1.79	1.74	0.50	0.20	0.68
decorin isoform b precursor [Homo sapiens]	24.40	0.68	0.58	0.57	0.88
decorin isoform c precursor [Homo sapiens]	24.40	0.68	0.58	0.57	0.88
decorin isoform d precursor [Homo sapiens]	16.24	0.65	0.29	0.12	0.41
immunoglobulin alpha Fc receptor isoform b precursor [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform c precursor [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform d [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform e [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform f [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform h [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
immunoglobulin alpha Fc receptor isoform i precursor [Homo sapiens]	7.95	1.53	0.95	0.55	0.92
DNA topoisomerase 2-beta [Homo sapiens]	0.45	1.19	1.44	5.02	1.64
major vault protein isoform 1 [Homo sapiens]	0.77	1.21	1.34	1.71	2.45
AP-2 complex subunit alpha-1 isoform 1 [Homo sapiens]	3.56	2.59	2.16	1.44	1.42
AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]	3.56	2.59	2.16	1.44	1.42
V-type proton ATPase catalytic subunit A [Homo sapiens]	1.57	1.17	1.44	1.28	1.82
V-type proton ATPase subunit B, kidney isoform [Homo sapiens]	2.49	0.95	0.90	0.65	0.84
V-type proton ATPase subunit B, brain isoform [Homo sapiens]	0.91	0.99	1.28	0.85	1.54
cytoskeleton-associated protein 4 [Homo sapiens]		6.17	9.85	20.93	6.71

serum paraoxonase/arylesterase 1 precursor [Homo sapiens]	0.23	0.79	0.26	0.13	0.25
importin subunit beta-1 isoform 1 [Homo sapiens]	1.34	0.93	1.27	1.79	2.30
hsc70-interacting protein isoform 1 [Homo sapiens]	22.13	1.18	2.35	2.69	1.63
ras-related protein Rab-6A isoform a [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
nuclear autoantigen Sp-100 isoform 2 [Homo sapiens]	0.35	0.97	0.91	3.22	1.86
ras-related protein Rab-5A isoform 1 [Homo sapiens]	0.35	1.42	2.17	3.39	1.74
echinoderm microtubule-associated protein-like 4 isoform a [Homo sapiens]	1.28	1.53	1.87	1.25	1.54
dihydropyrimidinase-related protein 5 [Homo sapiens]	1.57	5.64	1.21	0.92	3.14
BTB/POZ domain-containing protein KCTD12 [Homo sapiens]	0.64	0.94	0.51	0.31	0.64
protein disulfide-isomerase precursor [Homo sapiens]	0.75	1.42	2.60	1.91	2.01
transcription factor BTF3 isoform B [Homo sapiens]	1.00	0.98	0.83	0.46	2.30
nucleobindin-1 precursor [Homo sapiens]	1.82	1.79	2.16	0.81	2.30
protein kinase C beta type isoform 2 [Homo sapiens]	0.88	1.00	0.93	1.74	1.23
bifunctional purine biosynthesis protein PURH [Homo sapiens]	9.83	2.08	1.18	1.74	1.44
glycogenin-1 isoform 1 [Homo sapiens]	1.31	1.31	1.54	1.89	1.40
mitogen-activated protein kinase 11 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
EF-hand domain-containing protein D1 isoform 1 [Homo sapiens]	0.62	0.85	0.94	0.64	0.89
ferritin light chain [Homo sapiens]	3.26	1.76	2.54	2.17	2.27
porphobilinogen deaminase isoform 1 [Homo sapiens]	11.91	0.64	0.55	0.24	0.64
proline-serine-threonine phosphatase-interacting protein 1 [Homo sapiens]	4.38	0.99	1.00	0.98	0.92
ribosomal protein S6 kinase alpha-1 isoform a [Homo sapiens]	0.88	0.91	1.40	2.30	1.59
bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) [Homo sapiens]	1.31	2.08	1.00	0.77	1.82
NSFL1 cofactor p47 isoform a [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
EF-hand domain-containing protein D2 [Homo sapiens]	0.62	2.08	0.97	2.77	1.21
ketosamine-3-kinase [Homo sapiens]	3.93	0.85	0.69	0.61	0.68
aldose 1-epimerase [Homo sapiens]	1.00	0.80	0.43	0.31	0.53
core histone macro-H2A.1 isoform 1 [Homo sapiens]	2.38	1.19	0.88	0.62	0.75
histone H2B type 1-D [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
histone H2B type 1-J [Homo sapiens]	0.57	15.16	1.27	0.29	4.54
heme-binding protein 1 [Homo sapiens]	7.82	2.20	0.98	1.00	0.84
guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [Homo sapiens]	0.77	0.80	0.53	0.24	0.52
galectin-10 [Homo sapiens]	0.35	1.25	0.98	2.17	0.85
histone H2A.V isoform 2 [Homo sapiens]	0.35	5.03	0.79	0.55	0.82
mitogen-activated protein kinase 10 isoform 3 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 10 isoform 4 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 14 isoform 2 [Homo sapiens]	2.19	2.45	1.40	1.34	1.94
mitogen-activated protein kinase 14 isoform 3 [Homo sapiens]	2.38	2.45	1.40	1.34	1.94
mitogen-activated protein kinase 14 isoform 4 [Homo sapiens]	2.38	2.45	1.40	1.34	1.94
mitogen-activated protein kinase 8 isoform beta1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 8 isoform alpha2 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
ATP-dependent RNA helicase DDX39A [Homo sapiens]	1.57	1.25	1.27	0.94	0.99

stromal interaction molecule 1 isoform 2 precursor [Homo sapiens]	0.33	0.93	0.65	1.33	0.76
transcobalamin-1 precursor [Homo sapiens]	1.31	2.30	1.82	1.90	2.55
alpha-1B-glycoprotein precursor [Homo sapiens]	0.57	1.51	0.50	0.29	0.62
histone H2B type 1-C/E/F/G/I [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
mitogen-activated protein kinase 9 isoform alpha2 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 9 isoform alpha1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 9 isoform beta1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 9 isoform beta2 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
ARF GTPase-activating protein GIT2 isoform 3 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
SWI/SNF complex subunit SMARCC2 isoform a [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
EH domain-containing protein 4 [Homo sapiens]	2.15	0.38	0.88	1.63	0.64
spermine synthase isoform 1 [Homo sapiens]	2.00	0.98	0.75	0.63	0.85
scaffold attachment factor B1 isoform 3 [Homo sapiens]	0.52	1.25	3.48	7.80	1.40
peripherin [Homo sapiens]	0.75	0.28	0.28	0.52	0.22
cysteine--tRNA ligase, cytoplasmic isoform a [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
carcinoembryonic antigen-related cell adhesion molecule 8 precursor [Homo sapiens]	2.11	1.26	0.67	0.42	0.82
nucleosome assembly protein 1-like 1 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
versican core protein isoform 1 precursor [Homo sapiens]	1.18	6.12	0.70	0.42	0.92
calponin-1 [Homo sapiens]	0.91	0.79	0.95	1.66	1.47
26S protease regulatory subunit 6A [Homo sapiens]	0.98	0.92	0.54	0.44	0.52
retinal dehydrogenase 1 [Homo sapiens]	21.95	0.62	0.63	0.31	0.69
eukaryotic translation initiation factor 5 [Homo sapiens]	2.08	1.34	2.29	3.19	1.45
glycogen phosphorylase, brain form [Homo sapiens]	3.30	2.32	1.44	0.66	1.24
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform [Homo sapiens]	2.19	0.88	1.23	1.69	1.48
EH domain-containing protein 2 [Homo sapiens]	2.66	0.64	0.90	0.90	0.74
E3 ubiquitin-protein ligase NEDD4-like isoform 3 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
septin-6 isoform B [Homo sapiens]	1.44	0.94	1.39	1.54	1.74
toll-interacting protein [Homo sapiens]	0.91	2.59	0.98	0.85	2.68
phosphoglucomutase-1 isoform 1 [Homo sapiens]	0.98	0.95	1.90	1.59	0.98
protein disulfide-isomerase A3 precursor [Homo sapiens]	1.64	1.29	2.12	1.74	1.21
drebrin-like protein isoform a [Homo sapiens]	0.77	0.70	0.69	0.75	0.90
vacuolar protein sorting-associated protein VTA1 homolog isoform a [Homo sapiens]	2.83	1.51	1.87	1.31	1.55
spermatid perinuclear RNA-binding protein isoform 1 [Homo sapiens]	0.69	1.25	1.20	1.29	1.48
cullin-associated NEDD8-dissociated protein 1 [Homo sapiens]	5.56	0.89	1.69	2.38	1.18
PITH domain-containing protein 1 [Homo sapiens]	8.66	2.20	0.94	0.81	1.42
stathmin-4 isoform 1 [Homo sapiens]	0.77	0.94	3.60	7.80	1.58
attractin isoform 1 preproprotein [Homo sapiens]	0.39	0.92	0.40	0.24	0.54
attractin isoform 2 preproprotein [Homo sapiens]	0.39	0.92	0.40	0.24	0.54
14-3-3 protein gamma [Homo sapiens]	1.18	1.17	1.18	1.74	2.01

protein S100-A8 [Homo sapiens]	0.57	1.45	1.97	2.34	1.90
signal transducer and activator of transcription 3 isoform 2 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
signal transducer and activator of transcription 3 isoform 1 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
signal transducer and activator of transcription 5A isoform 1 [Homo sapiens]	0.45	0.68	1.19	1.98	0.76
signal transducer and activator of transcription 5B [Homo sapiens]	0.45	0.80	2.35	1.95	0.67
dual specificity mitogen-activated protein kinase kinase 3 isoform A [Homo sapiens]	0.95	0.77	0.68	0.52	0.81
dual specificity mitogen-activated protein kinase kinase 3 isoform B [Homo sapiens]	0.95	0.77	0.68	0.52	0.81
kallikrein-11 isoform 2 [Homo sapiens]	2.15	0.54	0.23	0.15	0.41
coactosin-like protein [Homo sapiens]	0.67	1.24	1.55	1.72	1.41
nudC domain-containing protein 2 [Homo sapiens]	1.61	0.78	0.44	0.38	0.51
apolipoprotein L1 isoform a precursor [Homo sapiens]	0.56	0.67	0.37	0.22	0.41
apolipoprotein L1 isoform b precursor [Homo sapiens]	0.56	0.67	0.37	0.22	0.41
malate dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	2.54	1.28	2.00	1.35	1.57
myotrophin [Homo sapiens]	3.08	0.96	1.26	1.76	1.21
programmed cell death 6-interacting protein isoform 1 [Homo sapiens]	1.82	0.80	1.54	2.51	0.77
septin-6 isoform A [Homo sapiens]	1.44	0.94	1.39	1.54	1.74
septin-6 isoform D [Homo sapiens]	1.44	0.94	1.39	1.54	1.74
apoptosis-associated speck-like protein containing a CARD isoform b [Homo sapiens]	2.38	1.26	1.87	2.44	1.81
apolipoprotein L3 isoform 1 [Homo sapiens]	0.56	0.67	0.31	0.19	0.53
apolipoprotein L3 isoform 3 [Homo sapiens]	0.56	0.67	0.31	0.19	0.53
apolipoprotein M isoform 1 [Homo sapiens]	0.26	0.57	0.30	0.18	0.45
annexin A11 isoform 1 [Homo sapiens]	0.88	1.24	2.16	0.96	1.44
prefoldin subunit 5 isoform alpha [Homo sapiens]	5.15	1.47	3.67	3.77	2.01
prefoldin subunit 5 isoform gamma [Homo sapiens]	5.15	1.47	3.67	3.77	2.01
high mobility group protein HMG-I/HMG-Y isoform a [Homo sapiens]	0.54	0.77	0.91	1.29	1.30
high mobility group protein HMG-I/HMG-Y isoform b [Homo sapiens]	0.66	0.80	0.75	0.76	2.53
cathepsin B preproprotein [Homo sapiens]	0.91	3.17	0.98	0.74	1.35
dipeptidyl peptidase 1 isoform b precursor [Homo sapiens]	1.93	2.31	3.99	3.12	2.45
cathepsin Z preproprotein [Homo sapiens]	0.43	1.37	1.24	1.35	1.48
proteasome subunit beta type-3 [Homo sapiens]	4.65	1.19	1.78	0.73	0.93
proteasome subunit beta type-4 [Homo sapiens]	2.54	2.08	1.72	0.74	0.98
tumor necrosis factor receptor superfamily member 10C precursor [Homo sapiens]	0.39	4.33	3.43	3.77	4.03
oxysterol-binding protein-related protein 9 isoform c [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
mixed lineage kinase domain-like protein isoform 1 [Homo sapiens]	0.56	0.54	3.12	5.69	3.40
actin-related protein 2/3 complex subunit 1A isoform 1 [Homo sapiens]	1.18	1.34	1.90	2.41	1.39
TIP41-like protein isoform 1 [Homo sapiens]	4.65	2.32	0.85	0.85	0.96
nesprin-1 isoform 2 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
proteasome subunit beta type-6 isoform 1 proprotein [Homo sapiens]	2.79	1.40	0.63	0.49	0.81
proteasome subunit alpha type-1 isoform 1 [Homo sapiens]	3.47	1.29	2.16	2.06	1.63
proteasome subunit alpha type-3 isoform 2 [Homo sapiens]	5.56	1.58	2.81	1.66	2.08

proteasome subunit alpha type-5 isoform 1 [Homo sapiens]	1.79	1.44	0.95	0.70	0.82
proteasome subunit alpha type-6 isoform a [Homo sapiens]	2.17	0.99	1.29	0.98	1.94
cathepsin S isoform 1 preproprotein [Homo sapiens]	0.35	1.34	2.56	0.78	1.56
sorting nexin-12 isoform 1 [Homo sapiens]	3.90	0.91	0.99	1.35	0.96
sorting nexin-1 isoform b [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
sorting nexin-1 isoform a [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
sorting nexin-2 isoform 1 [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
sorting nexin-3 isoform b [Homo sapiens]	5.15	1.62	1.57	3.41	2.34
prostaglandin E synthase 3 isoform a [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
signal recognition particle receptor subunit alpha isoform 1 [Homo sapiens]	0.91	1.44	1.39	1.27	1.18
copine-1 isoform a [Homo sapiens]	1.68	1.25	1.72	1.20	1.94
ubiquitin-like modifier-activating enzyme 1 [Homo sapiens]	2.02	0.98	0.97	0.92	0.94
transportin-1 isoform 2 [Homo sapiens]	2.38	0.68	1.23	2.81	1.48
acylamino-acid-releasing enzyme [Homo sapiens]	5.61	2.08	1.34	2.01	1.18
tropomyosin alpha-3 chain isoform 2 [Homo sapiens]	0.91	1.90	0.88	2.17	0.92
heat shock cognate 71 kDa protein isoform 2 [Homo sapiens]	1.64	2.71	0.92	0.75	0.96
interleukin enhancer-binding factor 3 isoform a [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
interleukin enhancer-binding factor 3 isoform b [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
interleukin enhancer-binding factor 3 isoform c [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
ribulose-phosphate 3-epimerase isoform 2 [Homo sapiens]	0.39	0.62	0.61	0.62	0.74
T-complex protein 1 subunit epsilon [Homo sapiens]	4.16	1.00	2.07	2.48	1.29
adipocyte plasma membrane-associated protein [Homo sapiens]	2.17	0.93	0.99	0.75	0.81
leucine-rich repeat-containing protein 47 [Homo sapiens]	1.64	2.32	2.13	3.32	1.81
protein kinase C and casein kinase substrate in neurons protein 1 [Homo sapiens]	0.88	1.96	2.58	5.06	2.28
costars family protein ABRACL [Homo sapiens]	1.64	0.96	0.73	0.62	0.83
protein phosphatase 1 regulatory subunit 21 isoform 2 [Homo sapiens]	2.27	1.38	3.90	0.69	0.61
WW domain-binding protein 2 [Homo sapiens]	2.46	0.93	0.70	0.61	0.70
26S protease regulatory subunit 4 [Homo sapiens]	5.11	1.96	1.96	1.48	1.81
26S protease regulatory subunit 6B isoform 2 [Homo sapiens]	4.40	1.31	0.82	0.51	0.81
keratin, type I cytoskeletal 16 [Homo sapiens]	1.93	1.62	3.16	1.23	5.13
reticulon-4 isoform B [Homo sapiens]	0.80	2.71	1.30	1.93	0.90
reticulon-4 isoform A [Homo sapiens]	0.80	2.71	1.30	1.93	0.90
piwi-like protein 2 [Homo sapiens]	7.02	2.20	0.74	0.43	0.64
26S protease regulatory subunit 8 isoform 1 [Homo sapiens]	7.36	0.85	0.62	0.62	0.58
endothelial differentiation-related factor 1 isoform beta [Homo sapiens]	0.56	0.85	0.95	0.97	1.82
signal recognition particle subunit SRP68 isoform 1 [Homo sapiens]	0.14	1.80	4.51	9.45	3.31
histone H2A type 2-C [Homo sapiens]	2.38	1.39	0.57	0.34	0.67
copine-8 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
copine-5 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
copine-7 isoform a [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
26S proteasome non-ATPase regulatory subunit 1 isoform 1 [Homo sapiens]	0.54	2.08	0.76	0.67	0.68

26S proteasome non-ATPase regulatory subunit 2 isoform 1 [Homo sapiens]	2.27	0.93	0.76	0.79	0.90
26S proteasome non-ATPase regulatory subunit 3 [Homo sapiens]	3.26	0.64	0.54	0.52	0.55
26S proteasome non-ATPase regulatory subunit 7 [Homo sapiens]	1.47	0.79	0.64	0.57	0.60
S-phase kinase-associated protein 1 isoform a [Homo sapiens]	12.32	1.26	2.10	1.42	1.35
S-phase kinase-associated protein 1 isoform b [Homo sapiens]	12.32	1.26	2.10	1.42	1.35
retinal dehydrogenase 2 isoform 1 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
retinal dehydrogenase 2 isoform 2 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
retinal dehydrogenase 2 isoform 3 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
aldehyde dehydrogenase X, mitochondrial precursor [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
aldehyde dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial isoform a precursor [Homo sapiens]	0.69	1.31	0.67	0.37	0.80
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 4 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 2 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 3 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 1 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 6 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
lamin isoform A [Homo sapiens]	0.16	0.08	0.14	0.05	0.13
lamin isoform A-delta10 [Homo sapiens]	0.16	0.08	0.14	0.05	0.13
voltage-gated potassium channel subunit beta-1 isoform 2 [Homo sapiens]	0.35	2.21	1.95	1.77	2.05
voltage-gated potassium channel subunit beta-1 isoform 3 [Homo sapiens]	0.35	2.21	1.95	1.77	2.05
voltage-gated potassium channel subunit beta-1 isoform 1 [Homo sapiens]	0.35	2.21	1.95	1.77	2.05
density-regulated protein [Homo sapiens]	0.88	0.45	0.39	0.41	0.45
protein BRICK1 [Homo sapiens]	0.52	1.93	1.62	2.21	1.90
unconventional myosin-Ib [Homo sapiens]	0.83	0.88	1.77	3.12	2.37
uncharacterized protein KIAA0825 isoform 2 [Homo sapiens]	0.35	0.69	0.31	0.18	0.49
huntingtin-interacting protein K isoform 1 [Homo sapiens]	0.25	0.66	2.29	1.00	0.78
MOB kinase activator 1B isoform 2 [Homo sapiens]	1.71	0.96	1.29	1.44	0.94
ficolin-3 isoform 1 precursor [Homo sapiens]	0.46	0.87	0.41	0.22	0.52
ficolin-3 isoform 2 precursor [Homo sapiens]	0.46	0.87	0.41	0.22	0.52
calpastatin isoform b [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
protein-tyrosine kinase 2-beta isoform b [Homo sapiens]	0.23	0.91	2.09	2.25	1.28
potassium voltage-gated channel subfamily H member 8 [Homo sapiens]		2.71	3.23	3.11	1.44
serpin B4 [Homo sapiens]	1.71	1.73	2.75	0.63	7.46
histone H2B type 3-B [Homo sapiens]	0.57	15.16	1.27	0.29	4.54
isocitrate dehydrogenase [NADP], mitochondrial isoform 1 precursor [Homo sapiens]	1.34	1.62	2.01	1.68	1.25
histone H2A type 2-B [Homo sapiens]	2.02	2.32	0.89	0.31	0.93
hemoglobin subunit gamma-1 [Homo sapiens]	65.18	0.77	0.66	0.19	0.76
unconventional myosin-XVIIIa isoform a [Homo sapiens]	1.37	2.20	0.88	1.98	0.97
ribose-phosphate pyrophosphokinase 3 [Homo sapiens]	9.70	0.82	0.76	0.84	0.88

sapiens]					
26S proteasome non-ATPase regulatory subunit 12 isoform 2 [Homo sapiens]	2.17	1.55	1.29	1.59	2.30
adenosine deaminase CECR1 isoform b [Homo sapiens]	0.80	0.97	0.99	0.79	0.73
exportin-2 isoform 1 [Homo sapiens]	1.18	0.89	0.97	1.56	2.39
inorganic pyrophosphatase 2, mitochondrial isoform 1 precursor [Homo sapiens]	1.64	2.59	2.15	1.59	0.93
phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapiens]	0.46	0.58	0.23	0.19	0.46
sulfotransferase 1A1 isoform a [Homo sapiens]	0.45	0.73	0.61	0.85	2.53
sulfotransferase 1A1 isoform b [Homo sapiens]	0.45	0.73	0.61	0.85	2.53
sulfotransferase family cytosolic 1B member 1 [Homo sapiens]	0.33	0.70	0.75	0.77	0.69
histone H2A.J [Homo sapiens]	1.41	1.77	0.53	0.24	0.79
protein phosphatase 1B isoform 2 [Homo sapiens]	0.62	0.89	0.58	0.52	0.96
protein phosphatase 1B isoform 3 [Homo sapiens]	0.33	0.88	1.29	2.05	1.26
NSFL1 cofactor p47 isoform b [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
U1 small nuclear ribonucleoprotein 70 kDa [Homo sapiens]	0.28	2.20	1.64	1.57	1.45
myosin regulatory light polypeptide 9 isoform a [Homo sapiens]	0.83	0.91	0.97	2.38	0.96
serine/threonine-protein phosphatase 2A activator isoform b [Homo sapiens]	9.83	1.00	1.18	1.25	0.89
tubulin beta chain isoform b [Homo sapiens]	1.21	0.76	1.60	0.71	0.84
protein phosphatase 1G [Homo sapiens]	0.54	0.91	0.80	0.68	0.75
alpha-adducin isoform a [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
alpha-adducin isoform b [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
alpha-adducin isoform c [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
alpha-adducin isoform d [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
eukaryotic translation initiation factor 2 subunit 2 [Homo sapiens]	15.50	0.85	0.82	0.54	0.99
serine/threonine-protein phosphatase 2A activator isoform a [Homo sapiens]	9.83	1.00	1.18	1.25	0.89
serine/threonine-protein phosphatase 2A activator isoform d [Homo sapiens]	9.83	1.40	1.19	1.25	2.30
copine-2 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
proteasome activator complex subunit 2 [Homo sapiens]	2.17	0.98	0.95	0.73	0.97
charged multivesicular body protein 1b [Homo sapiens]	1.61	0.74	1.21	4.33	1.88
coatamer subunit epsilon isoform a [Homo sapiens]	2.79	1.19	1.82	1.93	1.24
glycogen [starch] synthase, muscle isoform 1 [Homo sapiens]	0.54	1.00	0.77	0.57	0.76
inter-alpha-trypsin inhibitor heavy chain H4 isoform 1 precursor [Homo sapiens]	0.56	1.51	0.75	0.10	0.45
phosphoglycerate kinase 2 [Homo sapiens]	1.64	0.97	1.60	2.25	1.61
thrombospondin-4 precursor [Homo sapiens]	9.77	0.91	0.58	0.32	0.67
keratin, type I cytoskeletal 25 [Homo sapiens]	0.80	0.91	0.18	0.12	0.40
eukaryotic translation initiation factor 6 isoform c [Homo sapiens]	6.25	0.91	0.64	0.39	0.82
myosin regulatory light polypeptide 9 isoform b [Homo sapiens]	0.83	0.91	2.29	1.19	1.17
lipopolysaccharide-binding protein precursor [Homo sapiens]	0.98	1.98	2.68	0.77	0.88
phosphoribosylformylglycinamide synthase [Homo sapiens]	7.25	1.22	1.18	1.26	0.79
sorting nexin-27 [Homo sapiens]	0.75	0.94	0.93	1.26	0.98
SAP domain-containing ribonucleoprotein [Homo sapiens]	1.34	0.61	0.53	0.68	0.53

apolipoprotein C-II precursor [Homo sapiens]	0.14	0.48	0.31	0.08	0.28
B-cell receptor-associated protein 31 isoform b [Homo sapiens]	1.64	1.44	1.37	2.34	1.54
peroxiredoxin-2 [Homo sapiens]	141.98	0.96	1.51	0.39	1.46
ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]	4.84	2.59	1.34	0.66	0.58
olfactomedin-4 precursor [Homo sapiens]	1.37	1.89	1.56	1.25	2.77
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform b [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform a [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
peroxiredoxin-5, mitochondrial isoform b precursor [Homo sapiens]	1.79	0.94	1.31	1.54	1.21
peroxiredoxin-5, mitochondrial isoform c precursor [Homo sapiens]	2.46	1.30	1.53	1.58	1.18
peroxiredoxin-1 [Homo sapiens]	13.25	0.78	1.19	0.49	0.89
MAP kinase-activated protein kinase 2 isoform 2 [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
apoptotic protease-activating factor 1 isoform c [Homo sapiens]	0.77	0.85	1.68	1.37	1.29
apoptotic protease-activating factor 1 isoform d [Homo sapiens]	0.77	0.85	1.68	1.37	1.29
apoptotic protease-activating factor 1 isoform e [Homo sapiens]	0.75	0.92	1.34	2.11	1.82
thioredoxin-dependent peroxide reductase, mitochondrial isoform b [Homo sapiens]	1.47	1.45	1.82	2.30	1.81
serine/threonine-protein kinase PAK 2 [Homo sapiens]	0.80	0.67	0.70	0.57	0.68
neurofilament heavy polypeptide [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
adenosine kinase isoform a [Homo sapiens]	6.44	1.96	2.00	2.55	1.33
adenosine kinase isoform b [Homo sapiens]	6.44	1.96	2.00	2.55	1.33
opioid growth factor receptor [Homo sapiens]		1.94	2.57	2.59	0.68
cytoplasmic dynein 1 heavy chain 1 [Homo sapiens]	1.24	0.93	0.83	0.70	0.89
formin-like protein 1 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
tyrosine-protein phosphatase non-receptor type 11 isoform 1 [Homo sapiens]	0.98	0.97	2.49	1.92	1.81
phospholipid transfer protein isoform b precursor [Homo sapiens]	1.61	1.97	0.66	0.46	0.80
UPF0556 protein C19orf10 precursor [Homo sapiens]	1.18	1.73	2.54	1.94	1.39
thioredoxin reductase 1, cytoplasmic isoform 2 [Homo sapiens]	1.76	1.41	1.68	1.87	1.75
ras-related protein Rab-31 [Homo sapiens]	0.41	1.53	1.22	1.30	1.28
kinesin light chain 1 isoform 1 [Homo sapiens]	0.83	0.71	0.48	0.43	0.63
cAMP-dependent protein kinase catalytic subunit beta isoform 1 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
protein canopy homolog 3 precursor [Homo sapiens]	0.77	1.30	0.98	0.57	0.82
cofilin-2 isoform 1 [Homo sapiens]	0.91	1.26	1.55	1.72	1.38
guanine nucleotide-binding protein G(i) subunit alpha-1 isoform 1 [Homo sapiens]	2.00	1.19	2.02	2.08	1.34
nuclear pore complex protein Nup214 [Homo sapiens]	0.43	2.45	1.57	2.59	1.37
nuclease-sensitive element-binding protein 1 [Homo sapiens]	1.89	1.82	4.39	3.60	2.25
ras-related protein Rab-7a [Homo sapiens]	1.24	1.41	1.62	2.09	1.56
syntaxin-16 isoform b [Homo sapiens]	4.35	2.32	0.51	0.30	0.45
integrin alpha-X isoform 2 precursor [Homo sapiens]	0.31	1.21	0.68	0.41	0.71
phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein [Homo sapiens]	0.41	0.77	0.80	1.28	0.71
AP-3 complex subunit beta-2 isoform 2 [Homo sapiens]	0.77	2.30	1.42	0.45	2.60

ras-related protein Rab-27A [Homo sapiens]	2.38	1.19	1.40	3.26	1.28
importin subunit alpha-4 [Homo sapiens]	2.83	1.25	0.74	0.34	0.88
nck-associated protein 1-like isoform 1 [Homo sapiens]	9.83	1.74	0.76	0.80	1.45
adenylosuccinate synthetase isozyme 2 [Homo sapiens]	0.62	0.94	0.95	1.69	0.81
ras suppressor protein 1 isoform 2 [Homo sapiens]	1.76	2.59	1.54	0.98	1.54
nuclear factor NF-kappa-B p105 subunit isoform 1 [Homo sapiens]	1.96	0.55	0.40	0.24	0.44
fibulin-1 isoform C precursor [Homo sapiens]	0.75	1.40	0.43	0.22	0.53
fibulin-1 isoform D precursor [Homo sapiens]	0.43	1.96	0.76	0.31	0.60
heterogeneous nuclear ribonucleoprotein A3 [Homo sapiens]	0.77	0.97	1.34	1.75	1.34
stathmin-2 isoform 2 [Homo sapiens]	1.34	0.93	1.51	2.22	1.29
SUMO-conjugating enzyme UBC9 [Homo sapiens]	1.64	2.59	1.41	1.31	1.23
DCN1-like protein 1 [Homo sapiens]	12.38	1.34	1.87	2.28	1.34
BH3-interacting domain death agonist isoform 1 [Homo sapiens]	1.41	0.83	1.19	1.40	1.61
ADP-sugar pyrophosphatase [Homo sapiens]	3.08	0.85	0.96	1.26	1.74
lamin-B receptor [Homo sapiens]	0.46	0.89	0.96	2.49	1.30
erythrocyte band 7 integral membrane protein isoform b [Homo sapiens]	0.57	2.15	1.91	0.56	2.08
erythrocyte band 7 integral membrane protein isoform a [Homo sapiens]	0.57	2.15	1.91	0.56	2.08
deoxynucleoside triphosphate triphosphohydrolase SAMHD1 [Homo sapiens]	2.79	0.93	1.46	2.05	0.97
complement C5 preproprotein [Homo sapiens]	0.43	0.93	0.62	0.41	0.83
COP9 signalosome complex subunit 8 isoform 2 [Homo sapiens]	2.11	2.08	0.71	0.51	0.66
COP9 signalosome complex subunit 5 [Homo sapiens]	1.71	1.30	0.85	0.83	1.31
nucleoside diphosphate kinase A isoform a [Homo sapiens]	2.33	0.89	0.95	0.88	0.84
ubiquitin-like modifier-activating enzyme 7 [Homo sapiens]	0.39	0.88	0.88	0.89	1.28
U2 small nuclear ribonucleoprotein B'' [Homo sapiens]	0.33	1.36	1.51	2.62	1.75
small nuclear ribonucleoprotein-associated proteins B and B' isoform B' [Homo sapiens]	2.79	2.82	5.60	7.21	2.69
eukaryotic translation initiation factor 4 gamma 1 isoform 5 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
eukaryotic translation initiation factor 4 gamma 1 isoform 3 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
eukaryotic translation initiation factor 4 gamma 1 isoform 2 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
ribonuclease pancreatic precursor [Homo sapiens]	1.68	15.61	3.57	1.89	4.58
probable ATP-dependent RNA helicase DDX17 isoform 1 [Homo sapiens]	2.38	1.30	0.93	1.98	0.70
ELAV-like protein 1 [Homo sapiens]	0.69	1.54	2.16	3.42	2.34
neutral alpha-glucosidase AB isoform 2 precursor [Homo sapiens]	1.34	1.44	2.21	1.62	1.23
heat shock 70 kDa protein 4 [Homo sapiens]	2.19	1.40	0.93	1.23	0.97
interferon-induced guanylate-binding protein 2 [Homo sapiens]	0.66	1.40	2.41	3.92	1.57
citrate synthase, mitochondrial precursor [Homo sapiens]	1.68	0.92	0.98	0.65	0.93
suprabasin isoform 2 precursor [Homo sapiens]	0.69	0.93	0.88	0.31	0.94
COP9 signalosome complex subunit 4 isoform 1 [Homo sapiens]	4.38	1.22	2.47	1.69	2.30
neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	1.31	1.61	1.60	1.27	1.87
T-complex protein 1 subunit delta isoform a [Homo sapiens]	5.56	1.18	1.39	1.60	1.20

serpin B8 isoform a [Homo sapiens]	1.34	0.89	1.27	1.18	0.99
formin-binding protein 1 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
ATP-citrate synthase isoform 2 [Homo sapiens]	3.21	0.96	1.37	1.42	0.94
polypyrimidine tract-binding protein 3 isoform 1 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
sorcin isoform B [Homo sapiens]	14.12	0.75	0.66	0.69	1.61
ras-related protein Rab-6A isoform b [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
DNA helicase INO80 [Homo sapiens]	0.21	0.77	0.48	1.83	0.74
regulator complex protein LAMTOR5 [Homo sapiens]	0.54	2.70	4.82	5.63	3.41
pigment epithelium-derived factor precursor [Homo sapiens]	0.50	1.28	0.53	0.20	0.48
ras GTPase-activating-like protein IQGAP3 [Homo sapiens]	1.34	1.28	2.75	3.21	2.09
rho guanine nucleotide exchange factor 1 isoform 3 [Homo sapiens]	1.64	2.08	0.64	0.50	0.76
rho guanine nucleotide exchange factor 1 isoform 1 [Homo sapiens]	1.51	0.96	0.77	0.68	0.83
beta-arrestin-2 isoform 2 [Homo sapiens]	1.31	1.25	1.44	2.25	1.45
uncharacterized protein C9orf142 [Homo sapiens]	0.88	1.35	2.29	1.18	1.47
6-phosphogluconate dehydrogenase, decarboxylating [Homo sapiens]	0.98	1.19	1.53	2.06	1.37
cartilage oligomeric matrix protein precursor [Homo sapiens]	8.00	0.95	0.51	0.29	0.53
U5 small nuclear ribonucleoprotein 200 kDa helicase [Homo sapiens]	4.07	1.00	0.67	0.67	0.52
phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]	0.69	0.91	0.80	0.67	0.74
receptor-interacting serine/threonine-protein kinase 3 [Homo sapiens]	0.88	1.96	0.64	0.51	0.78
pre-mRNA 3'-end-processing factor FIP1 isoform 1 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
protein FAM107B isoform b [Homo sapiens]	0.66	0.99	1.20	1.88	0.97
7,8-dihydro-8-oxoguanine triphosphatase isoform p18 [Homo sapiens]	0.52	0.93	1.96	0.84	0.78
7,8-dihydro-8-oxoguanine triphosphatase isoform p22 [Homo sapiens]	0.52	0.93	1.96	0.84	0.78
aminopeptidase B [Homo sapiens]	2.38	0.88	1.22	1.53	0.94
thrombospondin-1 precursor [Homo sapiens]	7.25	2.46	0.81	0.44	1.42
nucleophosmin isoform 2 [Homo sapiens]	0.75	1.30	1.41	0.88	1.38
bisphosphoglycerate mutase [Homo sapiens]	10.27	2.20	0.61	0.41	0.68
2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 2 [Homo sapiens]	1.18	0.96	0.46	0.24	0.67
homeobox protein SIX5 [Homo sapiens]	0.46	1.34	2.05	2.61	1.74
ribulose-phosphate 3-epimerase isoform 1 [Homo sapiens]	0.39	0.62	0.61	0.62	0.74
nascent polypeptide-associated complex subunit alpha-2 [Homo sapiens]	1.00	0.82	0.69	0.29	0.83
charged multivesicular body protein 4a [Homo sapiens]	1.51	0.94	0.66	0.71	0.80
lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [Homo sapiens]	0.52	1.53	0.49	0.28	0.69
FYN-binding protein isoform 2 [Homo sapiens]	1.71	1.63	0.81	0.79	0.94
coatamer subunit epsilon isoform b [Homo sapiens]	2.79	1.19	1.82	1.93	1.24
coatamer subunit epsilon isoform c [Homo sapiens]	2.17	0.87	1.44	1.45	2.34
tumor protein D54 isoform e [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform f [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform a [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform b [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform c [Homo sapiens]	0.39	2.71	0.88	0.80	2.34

tumor protein D54 isoform d [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
ubiquitin-conjugating enzyme E2 variant 1 isoform a [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
TMEM189-UBE2V1 fusion protein [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
thymocyte nuclear protein 1 isoform 1 [Homo sapiens]	0.31	1.30	1.18	2.38	1.40
basic leucine zipper and W2 domain-containing protein 1 isoform 4 [Homo sapiens]	2.17	1.30	1.64	4.43	2.27
STE20-like serine/threonine-protein kinase [Homo sapiens]	0.66	0.91	1.21	2.34	0.88
fermitin family homolog 3 long form [Homo sapiens]	1.54	0.84	1.72	1.56	1.23
plectin isoform 1e [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1d [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1f [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1g [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1 [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1b [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
plectin isoform 1a [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
protein crumbs homolog 1 isoform 1 precursor [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
calponin-2 isoform b [Homo sapiens]	0.91	1.96	1.83	3.77	1.79
persulfide dioxygenase ETHE1, mitochondrial [Homo sapiens]	2.00	1.51	0.74	0.55	0.79
aflatoxin B1 aldehyde reductase member 2 [Homo sapiens]	2.83	0.88	1.20	1.98	0.92
probable ATP-dependent RNA helicase DDX46 [Homo sapiens]	0.95	0.78	0.96	2.21	0.88
prolyl endopeptidase [Homo sapiens]	1.44	0.84	0.99	1.93	0.98
glutamine-dependent NAD(+) synthetase [Homo sapiens]	2.27	1.90	3.41	2.30	1.86
putative RNA-binding protein Luc7-like 1 isoform b [Homo sapiens]	0.39	0.77	0.58	0.32	0.51
cytosol aminopeptidase [Homo sapiens]	1.47	1.19	1.21	0.83	2.01
reticulon-3 isoform c [Homo sapiens]	0.67	0.80	0.54	0.57	0.62
reticulon-3 isoform b [Homo sapiens]	0.67	0.80	0.54	0.57	0.62
ras-related protein Rab-5C isoform a [Homo sapiens]	0.77	2.27	4.15	6.77	1.52
60 kDa heat shock protein, mitochondrial [Homo sapiens]	1.00	0.78	1.36	0.71	0.73
histone H2A.V isoform 3 [Homo sapiens]	0.41	3.48	0.91	1.26	1.28
histone H2A.V isoform 5 [Homo sapiens]	0.28	4.03	0.68	1.37	1.21
rho-associated protein kinase 2 [Homo sapiens]	0.95	0.81	0.58	0.38	0.57
fatty acid synthase [Homo sapiens]	15.57	1.51	1.51	2.13	0.87
tropomyosin beta chain isoform 1 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
trans-Golgi network integral membrane protein 2 isoform 1 precursor [Homo sapiens]	0.25	0.95	0.71	0.52	0.76
vacuolar protein sorting-associated protein 13C isoform 1A [Homo sapiens]	0.07	1.37	0.81	0.46	0.54
heat shock protein 105 kDa isoform 1 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
complement factor D preproprotein [Homo sapiens]	1.37	1.72	0.44	0.29	0.58
dynammin-3 isoform a [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
U6 snRNA phosphodiesterase isoform 1 [Homo sapiens]	4.07	0.73	0.50	0.33	0.50
protein 4.1 isoform 2 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
protein 4.1 isoform 4 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
polymerase I and transcript release factor [Homo sapiens]	0.46	0.16	0.12	0.07	0.25
protein FAM49B [Homo sapiens]	0.98	0.92	0.90	1.21	1.88
long-chain-fatty-acid--CoA ligase 5 isoform a [Homo sapiens]	0.67	1.29	0.94	1.73	0.96

sapiens]					
long-chain-fatty-acid--CoA ligase 5 isoform b [Homo sapiens]	0.67	1.29	0.94	1.73	0.96
thioredoxin domain-containing protein 5 isoform 1 precursor [Homo sapiens]	1.00	1.62	1.47	1.70	1.30
unconventional myosin-XVIIIa isoform b [Homo sapiens]	1.37	2.20	0.88	1.98	0.97
ribonuclease inhibitor [Homo sapiens]	1.57	0.94	0.75	0.90	0.88
stathmin isoform a [Homo sapiens]	0.77	0.93	1.51	2.07	0.85
beta-soluble NSF attachment protein isoform b [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
polyadenylate-binding protein 3 [Homo sapiens]	0.62	1.51	1.00	2.38	0.99
WD repeat-containing protein 44 isoform 1 [Homo sapiens]	0.77	0.83	0.58	0.44	0.58
bcl-2-like protein 13 isoform a [Homo sapiens]	0.83	0.81	0.50	0.46	0.62
eosinophil cationic protein precursor [Homo sapiens]	0.80	1.21	0.84	0.60	0.76
growth factor receptor-bound protein 2 isoform 2 [Homo sapiens]	1.18	1.31	1.74	1.83	1.75
aspartate--tRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	2.66	2.08	1.80	2.30	1.56
mannose-1-phosphate guanylttransferase alpha [Homo sapiens]	1.64	0.95	1.51	1.72	1.24
complement component C7 precursor [Homo sapiens]	0.39	0.73	0.45	0.23	0.48
haptoglobin-related protein precursor [Homo sapiens]	0.77	1.35	0.82	0.43	1.18
protein dopey-2 [Homo sapiens]	0.33	0.69	0.96	0.69	0.65
serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 2 [Homo sapiens]	0.88	1.62	0.75	0.61	0.78
SAM and SH3 domain-containing protein 1 [Homo sapiens]	0.52	0.91	0.79	0.85	0.83
bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Homo sapiens]	3.30	0.97	1.21	0.57	2.53
protein unc-13 homolog D [Homo sapiens]	0.95	1.40	0.58	0.57	0.90
serine/threonine-protein phosphatase PP1-beta catalytic subunit isoform 1 [Homo sapiens]	2.70	1.62	0.99	0.68	1.23
rho-related GTP-binding protein RhoG precursor [Homo sapiens]	0.46	0.85	1.00	1.54	1.42
ras-related GTP-binding protein B short isoform [Homo sapiens]	0.77	0.89	0.40	0.27	0.58
ras-related GTP-binding protein B long isoform [Homo sapiens]	0.77	0.89	0.40	0.27	0.58
transcription elongation factor B polypeptide 2 isoform b [Homo sapiens]	1.47	1.21	1.27	1.52	1.81
hydrocephalus-inducing protein homolog isoform b [Homo sapiens]	0.39	2.08	0.38	0.19	0.54
polyadenylate-binding protein 1 [Homo sapiens]	0.62	1.51	1.00	2.38	0.99
tubulin alpha-3E chain [Homo sapiens]	0.75	0.71	0.69	0.46	0.78
cAMP-dependent protein kinase catalytic subunit alpha isoform 2 [Homo sapiens]	0.91	0.69	0.78	1.00	0.80
cAMP-dependent protein kinase catalytic subunit beta isoform 3 [Homo sapiens]	1.31	0.83	1.27	1.52	0.98
adenosine deaminase [Homo sapiens]	1.79	2.45	1.36	1.73	1.36
lysophosphatidylcholine acyltransferase 2 [Homo sapiens]	0.45	1.22	1.78	2.32	0.92
nebulette isoform 2 [Homo sapiens]	0.54	0.87	1.21	0.89	1.61
fibronectin isoform 7 preproprotein [Homo sapiens]	0.50	1.64	0.73	0.90	1.71
fibronectin isoform 6 preproprotein [Homo sapiens]	0.69	1.44	0.70	0.74	1.37
fibronectin isoform 5 preproprotein [Homo sapiens]	0.69	1.44	0.70	0.74	1.37
fibronectin isoform 4 preproprotein [Homo sapiens]	0.69	1.42	0.70	0.74	1.38
fibronectin isoform 1 preproprotein [Homo sapiens]	0.67	1.41	0.70	0.79	1.37
cAMP-dependent protein kinase type I-alpha	0.64	1.62	0.82	0.79	0.89

regulatory subunit isoform a [Homo sapiens]					
keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	0.77	0.63	0.27	0.15	0.50
S-methyl-5'-thioadenosine phosphorylase [Homo sapiens]	6.36	1.40	0.98	1.21	1.54
protein kinase C beta type isoform 1 [Homo sapiens]	0.88	1.00	0.93	1.74	1.23
tryptophan--tRNA ligase, cytoplasmic isoform b [Homo sapiens]	1.96	0.74	1.78	0.93	0.92
signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
reticulon-4 isoform D [Homo sapiens]	0.80	2.71	1.30	1.93	0.90
tropomyosin beta chain isoform 2 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
neutrophil cytosol factor 4 isoform 1 [Homo sapiens]	2.38	0.79	0.89	1.30	0.85
serine protease 57 precursor [Homo sapiens]	1.82	0.87	0.51	0.37	0.70
plectin isoform 1c [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
syntaxin-16 isoform a [Homo sapiens]	4.35	2.32	0.51	0.30	0.45
minor histocompatibility protein HA-1 isoform 1 precursor [Homo sapiens]	0.45	0.68	0.50	0.79	0.75
alpha-soluble NSF attachment protein [Homo sapiens]	1.89	0.94	0.90	1.18	1.42
glucosidase 2 subunit beta isoform 1 precursor [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
transgelin [Homo sapiens]	1.28	2.45	0.60	0.35	0.88
non-histone chromosomal protein HMG-14 [Homo sapiens]	0.33	1.18	1.56	2.71	1.74
CD44 antigen isoform 1 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 2 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 3 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 4 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 5 precursor [Homo sapiens]	0.50	3.10	1.29	1.26	1.37
UTP--glucose-1-phosphate uridylyltransferase isoform a [Homo sapiens]	2.79	1.62	1.31	1.42	1.23
mitogen-activated protein kinase 12 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
SAM domain-containing protein SAMSN-1 isoform 1 [Homo sapiens]	0.19	1.47	0.79	0.85	0.83
6-phosphofructokinase, liver type isoform b [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
T-complex protein 1 subunit theta isoform 1 [Homo sapiens]	3.47	1.26	0.98	1.34	1.35
collagen alpha-2(I) chain precursor [Homo sapiens]	1.21	2.34	2.10	0.49	3.41
eukaryotic translation initiation factor 4B [Homo sapiens]	3.75	1.22	1.18	0.95	1.26
glutathione reductase, mitochondrial isoform 1 precursor [Homo sapiens]	1.79	2.45	1.22	2.73	1.27
hematological and neurological expressed 1 protein isoform 2 [Homo sapiens]	0.39	0.82	1.72	2.27	0.53
ATP synthase subunit alpha, mitochondrial isoform c [Homo sapiens]	2.46	0.88	1.37	0.64	0.68
ATP synthase subunit alpha, mitochondrial isoform a precursor [Homo sapiens]	2.46	0.88	1.37	0.64	0.68
alpha-1-antitrypsin precursor [Homo sapiens]	0.54	2.48	1.27	0.77	1.50
small ubiquitin-related modifier 4 [Homo sapiens]	0.64	1.73	1.18	1.77	2.34
tubulin-folding cofactor B [Homo sapiens]	1.41	0.89	1.30	1.98	1.61
microtubule-associated protein 1S [Homo sapiens]	1.31	0.99	0.87	1.18	0.99
thioredoxin isoform 1 [Homo sapiens]	3.52	0.97	2.69	1.51	1.41
U2 small nuclear ribonucleoprotein A' [Homo sapiens]	0.98	1.21	1.75	2.61	1.53
phosphoglycerate mutase 2 [Homo sapiens]	0.88	1.62	1.38	1.44	1.17
alpha-1-antichymotrypsin precursor [Homo sapiens]	0.77	1.57	0.65	0.46	0.84
low affinity immunoglobulin gamma Fc region receptor	0.54	2.31	1.74	2.45	7.01

III-A isoform a precursor [Homo sapiens]

annexin A2 isoform 1 [Homo sapiens]	1.68	0.54	1.58	0.42	1.29
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform isoform a [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
heterogeneous nuclear ribonucleoprotein D0 isoform d [Homo sapiens]	0.50	0.96	1.29	2.11	1.28
protein SPT2 homolog [Homo sapiens]	1.28	0.77	0.42	0.95	0.67
lysosomal alpha-mannosidase isoform 1 precursor [Homo sapiens]	3.61	1.79	1.26	0.66	1.35
sulfhydryl oxidase 1 isoform b precursor [Homo sapiens]	1.31	1.94	0.93	1.33	1.41
annexin A13 isoform a [Homo sapiens]	0.69	2.45	0.84	0.68	1.23
annexin A13 isoform b [Homo sapiens]	0.69	2.45	0.84	0.68	1.23
G protein-coupled receptor kinase 6 isoform B [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
G protein-coupled receptor kinase 6 isoform C [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
G protein-coupled receptor kinase 6 isoform A [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
E3 ubiquitin-protein ligase CBL [Homo sapiens]	2.00	0.70	0.57	0.59	0.61
endoplasmic reticulum resident protein 44 precursor [Homo sapiens]	1.31	2.15	3.26	3.60	2.08
HLA class I histocompatibility antigen, Cw-1 alpha chain precursor [Homo sapiens]	0.83	0.96	0.67	0.34	0.80
heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]	0.62	0.82	1.21	0.98	0.88
heterogeneous nuclear ribonucleoprotein L isoform b [Homo sapiens]	0.62	0.82	0.73	0.98	0.87
actin-related protein 2 isoform a [Homo sapiens]	0.75	1.00	0.99	0.77	0.89
WD repeat-containing protein 1 isoform 2 [Homo sapiens]	0.83	1.51	1.41	0.99	1.45
histone H3.2 [Homo sapiens]	0.77	4.79	0.79	0.39	1.71
splicing factor 3B subunit 1 isoform 1 [Homo sapiens]	0.91	0.80	0.41	0.27	0.53
splicing factor 3B subunit 3 [Homo sapiens]	0.80	0.94	0.62	0.75	0.78
translational activator GCN1 [Homo sapiens]	1.31	0.96	0.74	0.62	0.80
lactotransferrin isoform 1 precursor [Homo sapiens]	0.77	5.05	0.84	1.31	2.38
small ubiquitin-related modifier 2 isoform a precursor [Homo sapiens]	1.64	0.99	1.22	1.47	0.99
small ubiquitin-related modifier 2 isoform b precursor [Homo sapiens]	1.64	0.99	1.22	1.47	0.99
complement factor H-related protein 3 isoform 1 precursor [Homo sapiens]	0.33	1.38	0.90	0.53	0.94
RNA-binding protein 25 [Homo sapiens]		4.31	1.43	6.14	1.39
collagen alpha-3(VI) chain isoform 1 precursor [Homo sapiens]	2.15	1.79	0.52	0.32	0.90
collagen alpha-3(VI) chain isoform 5 precursor [Homo sapiens]	2.15	1.79	0.52	0.32	0.90
retinol-binding protein 4 precursor [Homo sapiens]	0.39	0.49	0.17	0.12	0.54
ribosomal protein S6 kinase alpha-1 isoform b [Homo sapiens]	0.88	0.91	1.40	2.30	1.59
syntenin-1 isoform 1 [Homo sapiens]	0.52	0.77	0.31	0.13	0.42
syntenin-1 isoform 2 [Homo sapiens]	0.52	0.77	0.31	0.13	0.42
syntenin-1 isoform 3 [Homo sapiens]	0.52	0.77	0.31	0.13	0.42
disco-interacting protein 2 homolog B [Homo sapiens]	0.21	1.35	0.66	0.78	1.26
desmin [Homo sapiens]	0.57	0.45	0.35	0.51	0.35
C-reactive protein precursor [Homo sapiens]	2.00	7.92	9.06	2.53	1.73
pre-mRNA-splicing factor SYF1 [Homo sapiens]	0.21	0.66	0.30	0.16	0.54
AMP deaminase 2 isoform 3 [Homo sapiens]	1.34	0.88	0.66	0.75	0.91

nucleolin [Homo sapiens]	0.77	0.91	1.22	1.78	1.81
keratin, type I cytoskeletal 9 [Homo sapiens]	2.31	0.89	0.35	0.25	0.43
unconventional myosin-1e [Homo sapiens]	0.83	0.74	0.66	1.45	0.97
amyloid beta A4 precursor protein-binding family B member 1-interacting protein [Homo sapiens]	0.62	0.91	1.34	1.90	0.83
nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 [Homo sapiens]	1.51	1.21	2.32	4.27	1.94
dynamin-1 isoform 2 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
dynamin-2 isoform 3 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
dynamin-2 isoform 1 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
dynamin-2 isoform 2 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
dynamin-2 isoform 4 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
septin-2 isoform a [Homo sapiens]	3.39	1.51	2.69	0.59	0.87
U4/U6.U5 tri-snRNP-associated protein 2 isoform 1 [Homo sapiens]	0.41	1.34	1.42	1.80	1.25
mitotic checkpoint protein BUB3 isoform b [Homo sapiens]	2.00	1.24	0.56	0.37	0.90
regulator complex protein LAMTOR4 [Homo sapiens]	3.34	2.54	2.69	0.71	1.18
rho GDP-dissociation inhibitor 2 [Homo sapiens]	0.64	1.22	1.48	1.56	1.29
ferritin heavy chain [Homo sapiens]	2.38	2.48	2.10	2.32	1.60
RNA-binding motif protein, X chromosome isoform 1 [Homo sapiens]	1.31	0.94	2.16	1.97	0.93
complement C1q subcomponent subunit C precursor [Homo sapiens]	0.56	1.17	0.52	0.30	0.69
phosphatidylinositol-binding clathrin assembly protein isoform 1 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
phosphatidylinositol-binding clathrin assembly protein isoform 2 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 3 [Homo sapiens]	0.88	1.62	0.75	0.61	0.78
tubulin alpha-1B chain [Homo sapiens]	1.00	0.73	0.99	0.51	0.84
cullin-4A isoform 1 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
T-complex protein 1 subunit alpha isoform a [Homo sapiens]	2.08	1.62	0.96	1.21	1.00
T-complex protein 1 subunit alpha isoform b [Homo sapiens]	2.58	2.45	0.79	0.53	0.93
calmodulin [Homo sapiens]	1.57	1.65	1.88	1.70	2.20
bcl-2-like protein 15 [Homo sapiens]	0.98	0.96	2.56	1.28	0.92
T-complex protein 1 subunit zeta isoform b [Homo sapiens]	4.99	1.26	1.34	2.24	1.63
T-complex protein 1 subunit zeta-2 isoform 1 [Homo sapiens]	2.79	0.97	2.29	1.57	1.63
T-complex protein 1 subunit eta isoform b [Homo sapiens]	2.11	1.24	0.89	0.74	0.91
fetuin-B precursor [Homo sapiens]	0.33	0.71	0.40	0.22	0.50
destrin isoform b [Homo sapiens]	0.31	0.79	0.95	1.41	2.60
T-complex protein 1 subunit gamma isoform c [Homo sapiens]	2.49	1.62	0.99	1.28	1.74
heterogeneous nuclear ribonucleoprotein A1-like 2 [Homo sapiens]	1.96	1.62	1.27	1.34	0.97
obg-like ATPase 1 isoform 1 [Homo sapiens]	11.64	1.30	1.29	1.89	2.60
obg-like ATPase 1 isoform 2 [Homo sapiens]	5.93	0.97	0.95	0.85	0.90
dynamin-1 isoform 1 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
filaggrin [Homo sapiens]	10.91	0.82	0.84	0.15	0.57
calcyclin-binding protein isoform 2 [Homo sapiens]	1.34	1.39	2.73	3.92	1.83
splicing factor U2AF 65 kDa subunit isoform b [Homo sapiens]	1.71	1.40	2.56	1.89	1.20
putative ubiquitin-conjugating enzyme E2 N-like [Homo sapiens]	9.70	1.44	2.68	2.38	2.01

abl interactor 1 isoform a [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform b [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform c [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform d [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
ficolin-2 isoform a precursor [Homo sapiens]	0.54	1.22	0.82	0.49	1.45
heterogeneous nuclear ribonucleoprotein C-like 1 [Homo sapiens]	0.98	2.45	1.63	3.87	1.62
drebrin-like protein isoform b [Homo sapiens]	0.77	0.70	0.69	0.75	0.90
protein CutA isoform 1 [Homo sapiens]	1.44	1.18	0.88	0.82	0.89
cysteine--tRNA ligase, cytoplasmic isoform c [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
bifunctional glutamate/proline--tRNA ligase [Homo sapiens]	0.28	1.26	4.36	5.53	1.92
insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]	2.38	1.39	0.96	0.73	1.31
insulin-like growth factor-binding protein 3 isoform a precursor [Homo sapiens]	2.38	1.39	0.96	0.73	1.31
exocyst complex component 6 isoform b [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
SAFB-like transcription modulator isoform b [Homo sapiens]		1.22	15.13	17.04	8.40
dipeptidyl peptidase 2 preproprotein [Homo sapiens]	0.91	1.59	0.98	0.65	1.23
integrin alpha-D precursor [Homo sapiens]	0.31	1.21	0.68	0.41	0.71
complement factor H isoform a precursor [Homo sapiens]	0.41	0.99	0.58	0.30	0.74
complement factor H isoform b precursor [Homo sapiens]	0.41	1.00	0.57	0.29	0.75
C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	0.67	1.30	0.61	0.38	0.81
caspase recruitment domain-containing protein 16 isoform 1 [Homo sapiens]	0.41	0.77	0.56	0.91	0.63
phosphoglucomutase-2 [Homo sapiens]	1.44	1.19	1.21	1.30	1.21
beta-actin-like protein 2 [Homo sapiens]	0.88	0.93	0.68	0.66	0.82
T-complex protein 1 subunit gamma isoform a [Homo sapiens]	2.76	1.25	1.43	1.56	1.48
SAFB-like transcription modulator isoform a [Homo sapiens]		1.22	15.13	17.04	8.40
tropomyosin alpha-1 chain isoform 6 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform a [Homo sapiens]	0.69	0.91	0.80	0.67	0.74
exocyst complex component 6 isoform a [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
plasminogen activator inhibitor 1 RNA-binding protein isoform 1 [Homo sapiens]	2.79	1.68	3.19	4.75	1.60
plasminogen activator inhibitor 1 RNA-binding protein isoform 2 [Homo sapiens]	2.79	1.68	3.19	4.75	1.60
plasminogen activator inhibitor 1 RNA-binding protein isoform 3 [Homo sapiens]	2.79	1.68	3.19	4.75	1.60
plasminogen activator inhibitor 1 RNA-binding protein isoform 4 [Homo sapiens]	2.79	1.68	3.19	4.75	1.60
vacuolar protein sorting-associated protein 13C isoform 2A [Homo sapiens]	0.07	1.37	0.81	0.46	0.54
vacuolar protein sorting-associated protein 13C isoform 2B [Homo sapiens]	0.07	1.37	0.81	0.46	0.54
complement C1r subcomponent precursor [Homo sapiens]	0.54	1.53	1.00	0.49	0.82
vacuolar protein sorting-associated protein 13C isoform 1B [Homo sapiens]	0.07	1.37	0.81	0.46	0.54
NEDD8-activating enzyme E1 regulatory subunit isoform b [Homo sapiens]	2.34	1.22	1.37	1.64	1.20
NME1-NME2 protein [Homo sapiens]	4.02	1.62	2.40	2.38	2.19
histone H2B type 2-F isoform a [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
mitogen-activated protein kinase 1 [Homo sapiens]	2.19	1.62	3.12	4.57	2.34

alpha-2-macroglobulin precursor [Homo sapiens]	0.80	0.91	0.45	0.25	0.75
porphobilinogen deaminase isoform 2 [Homo sapiens]	11.91	0.64	0.55	0.24	0.64
inosine-5'-monophosphate dehydrogenase 2 [Homo sapiens]	1.00	0.81	0.77	1.98	0.82
protein PML isoform 1 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
protein PML isoform 2 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
protein PML isoform 11 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
neutrophil cytosol factor 2 isoform 1 [Homo sapiens]	0.75	0.71	0.77	0.87	0.80
proteoglycan 4 isoform A precursor [Homo sapiens]	0.54	2.32	0.70	0.41	0.79
complement C4-A isoform 1 preproprotein [Homo sapiens]	0.35	0.93	0.52	0.30	0.77
SH3 domain-containing kinase-binding protein 1 isoform b [Homo sapiens]	2.00	1.25	1.48	2.06	1.28
superoxide dismutase [Mn], mitochondrial isoform A precursor [Homo sapiens]	0.66	1.30	0.88	0.61	1.23
superoxide dismutase [Mn], mitochondrial isoform B precursor [Homo sapiens]	0.66	1.30	0.88	0.61	1.23
complement factor B preproprotein [Homo sapiens]	0.39	1.90	0.64	0.33	0.70
actin-related protein 2/3 complex subunit 4 isoform b [Homo sapiens]	0.77	1.51	2.30	3.62	1.39
proteasome subunit alpha type-7-like isoform 1 [Homo sapiens]	4.65	1.37	2.13	1.54	1.58
proteasome subunit alpha type-7-like isoform 2 [Homo sapiens]	4.65	1.37	2.13	1.54	1.58
proteasome subunit alpha type-7-like isoform 3 [Homo sapiens]	4.65	1.37	2.13	1.54	1.58
CUGBP Elav-like family member 2 isoform 1 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
CUGBP Elav-like family member 2 isoform 3 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
tryptase beta-2 preproprotein [Homo sapiens]	1.31	0.62	0.37	0.40	0.43
cytochrome b-245 light chain [Homo sapiens]	0.69	1.57	3.54	0.97	1.52
putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]	2.79	0.94	1.96	1.18	0.78
AP-2 complex subunit mu isoform b [Homo sapiens]	1.31	1.40	0.69	0.64	0.84
HCLS1-binding protein 3 [Homo sapiens]	1.18	0.54	0.57	0.70	0.49
ATP-binding cassette sub-family F member 1 isoform a [Homo sapiens]	2.79	2.59	0.89	0.75	0.92
inter-alpha-trypsin inhibitor heavy chain H2 precursor [Homo sapiens]	0.46	0.51	0.24	0.14	0.40
ankyrin-1 isoform 4 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
ankyrin-1 isoform 2 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
ankyrin-1 isoform 3 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
ankyrin-1 isoform 1 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
peptidase inhibitor 16 precursor [Homo sapiens]	0.16	1.58	0.39	0.27	0.62
AMP deaminase 3 isoform 1C [Homo sapiens]	1.44	0.85	0.80	0.83	0.81
fibrinogen beta chain isoform 1 preproprotein [Homo sapiens]	1.61	1.93	1.36	1.22	3.53
fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]	2.19	2.53	1.90	1.69	5.87
fibrinogen gamma chain isoform gamma-B precursor [Homo sapiens]	2.19	2.53	1.90	1.69	5.87
delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor [Homo sapiens]	0.57	1.28	2.05	1.26	1.25
glycogen phosphorylase, liver form isoform 1 [Homo sapiens]	0.67	0.91	1.51	1.30	1.39
rho GTPase-activating protein 30 isoform 1 [Homo sapiens]	0.10	1.17	2.29	1.78	0.98
cell surface glycoprotein MUC18 precursor [Homo sapiens]	0.28	1.18	0.35	0.20	0.53

phosphoglycerate mutase 4 [Homo sapiens]	1.24	2.71	1.39	1.44	2.68
myeloblastin precursor [Homo sapiens]	1.21	1.42	0.98	0.84	1.36
alcohol dehydrogenase class-3 [Homo sapiens]	1.64	0.83	1.43	0.92	0.90
AP-1 complex subunit gamma-1 isoform b [Homo sapiens]	0.43	0.78	0.87	1.23	0.75
AP-1 complex subunit gamma-1 isoform a [Homo sapiens]	0.43	0.78	0.87	1.23	0.75
apolipoprotein A-IV precursor [Homo sapiens]	0.14	0.29	0.13	0.06	0.12
adenine phosphoribosyltransferase isoform b [Homo sapiens]	4.65	1.24	1.69	2.58	1.52
annexin A6 isoform 1 [Homo sapiens]	0.91	2.01	1.65	1.79	1.56
serine/arginine-rich splicing factor 7 isoform 1 [Homo sapiens]	1.68	0.67	0.45	0.43	0.66
TIP41-like protein isoform 2 [Homo sapiens]	4.65	2.32	0.85	0.85	0.96
serpin B8 isoform b [Homo sapiens]	1.79	0.77	1.36	1.35	0.93
proteasome subunit beta type-8 isoform E2 proprotein [Homo sapiens]	0.88	0.91	0.76	0.73	0.75
thymopoietin isoform gamma [Homo sapiens]	0.66	0.81	0.49	0.30	0.66
thymopoietin isoform beta [Homo sapiens]	0.66	0.81	0.49	0.30	0.66
ubiquitin-conjugating enzyme E2 variant 1 isoform d [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
corticosteroid-binding globulin precursor [Homo sapiens]	0.56	1.90	0.51	0.27	0.70
heparin cofactor 2 precursor [Homo sapiens]	0.45	0.64	0.45	0.32	0.85
plasma protease C1 inhibitor precursor [Homo sapiens]	0.57	1.27	0.77	0.42	1.23
serine protease inhibitor Kazal-type 5 isoform b precursor [Homo sapiens]	5.15	2.08	0.69	0.49	1.42
plasminogen-like protein B precursor [Homo sapiens]	0.10	0.28	0.18	0.05	0.20
LDLR chaperone MESD precursor [Homo sapiens]	2.00	1.37	1.40	1.38	1.54
heterogeneous nuclear ribonucleoprotein U isoform a [Homo sapiens]	0.77	0.89	1.69	2.31	1.23
glutamine synthetase [Homo sapiens]	0.88	1.51	1.68	2.51	1.21
matrix metalloproteinase-9 preproprotein [Homo sapiens]	0.88	1.55	1.64	2.06	2.01
translocator protein [Homo sapiens]	0.69	0.80	2.56	1.27	0.61
probable ubiquitin carboxyl-terminal hydrolase FAF-Y [Homo sapiens]	1.54	0.91	0.58	0.67	0.77
BRISC and BRCA1-A complex member 1 isoform 1 [Homo sapiens]	1.61	2.52	2.56	4.18	2.74
phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform A precursor [Homo sapiens]	1.57	0.93	0.75	0.54	0.76
protein phosphatase 1B isoform 4 [Homo sapiens]	0.62	0.89	0.58	0.52	0.96
protein phosphatase 1B isoform 5 [Homo sapiens]	0.62	0.89	0.58	0.52	0.96
very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]	0.31	0.65	0.75	0.39	0.62
staphylococcal nuclease domain-containing protein 1 [Homo sapiens]	1.41	0.79	0.48	0.43	0.68
endoplasmic reticulum resident protein 29 isoform 2 precursor [Homo sapiens]	0.83	1.57	3.19	2.37	1.63
inorganic pyrophosphatase 2, mitochondrial isoform 2 precursor [Homo sapiens]	1.64	2.59	2.15	1.59	0.93
inorganic pyrophosphatase 2, mitochondrial isoform 3 precursor [Homo sapiens]	1.64	2.59	2.15	1.59	0.93
plasma kallikrein preproprotein [Homo sapiens]	0.33	0.62	0.29	0.18	0.43
exocyst complex component 4 isoform a [Homo sapiens]	0.25	0.65	0.27	0.15	0.65
exocyst complex component 4 isoform b [Homo sapiens]	0.25	0.65	0.27	0.15	0.65
AP-5 complex subunit zeta-1 [Homo sapiens]	0.77	0.78	0.90	0.74	0.94

cytoplasmic FMR1-interacting protein 2 isoform a [Homo sapiens]	2.17	0.96	0.93	2.32	1.33
E3 ubiquitin-protein ligase UBR4 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
ubiquitin carboxyl-terminal hydrolase 14 isoform b [Homo sapiens]	19.15	0.91	1.58	1.96	1.18
thymocyte nuclear protein 1 isoform 2 [Homo sapiens]	0.31	1.30	1.18	2.38	1.40
eukaryotic translation initiation factor 3 subunit J isoform 1 [Homo sapiens]	4.19	0.88	0.93	2.51	2.45
gasdermin-D [Homo sapiens]	0.52	1.80	1.26	0.88	1.35
nucleophosmin isoform 3 [Homo sapiens]	0.67	1.51	1.94	1.64	1.52
transcription factor BTF3 isoform A [Homo sapiens]	1.00	0.98	0.83	0.46	2.30
eukaryotic translation initiation factor 3 subunit C isoform a [Homo sapiens]	2.15	1.34	1.75	1.78	1.37
eukaryotic initiation factor 4A-II [Homo sapiens]	1.31	0.89	0.58	0.45	0.73
eukaryotic translation initiation factor 5B [Homo sapiens]	1.96	1.28	1.00	0.89	0.94
ribose-phosphate pyrophosphokinase 2 isoform 1 [Homo sapiens]	9.42	0.83	0.70	0.69	0.84
UPF0687 protein C20orf27 isoform 1 [Homo sapiens]	4.19	1.37	2.56	1.81	1.25
EGF-containing fibulin-like extracellular matrix protein 1 precursor [Homo sapiens]	0.57	2.39	0.45	0.23	0.63
complement receptor type 1 isoform F precursor [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
complement receptor type 1 isoform S precursor [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
V-type proton ATPase subunit E 1 isoform b [Homo sapiens]	0.43	0.78	0.82	0.85	0.62
collagen alpha-1(VI) chain precursor [Homo sapiens]	1.76	0.91	0.55	0.45	0.85
ATP-dependent RNA helicase DDX3X isoform 1 [Homo sapiens]	0.83	0.77	0.92	1.62	0.92
complement C1q subcomponent subunit B precursor [Homo sapiens]	0.54	1.62	0.53	0.30	0.62
integrin alpha-M isoform 2 precursor [Homo sapiens]	1.24	1.51	0.98	0.49	0.92
vasorin precursor [Homo sapiens]	0.52	1.51	0.69	0.39	0.68
sorting nexin-6 isoform b [Homo sapiens]	1.18	2.32	1.00	0.87	0.92
sorting nexin-6 isoform a [Homo sapiens]	1.18	2.32	1.00	0.87	0.92
copine-9 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
complement component C1q receptor precursor [Homo sapiens]	2.66	2.18	1.27	1.38	1.72
vitronectin precursor [Homo sapiens]	0.46	0.58	0.50	0.24	0.70
neutral alpha-glucosidase AB isoform 3 precursor [Homo sapiens]	1.37	1.24	1.72	1.27	1.29
myosin light polypeptide 6 isoform 2 [Homo sapiens]	0.77	0.94	1.29	1.52	2.01
integrin beta-2 precursor [Homo sapiens]	0.43	0.89	0.61	0.37	0.90
von Willebrand factor preproprotein [Homo sapiens]	0.75	1.73	1.38	0.85	1.20
cell division control protein 42 homolog isoform 1 precursor [Homo sapiens]	1.00	2.08	1.44	1.74	1.23
phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform B precursor [Homo sapiens]	1.57	0.93	0.75	0.54	0.76
phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform C precursor [Homo sapiens]	1.57	0.93	0.75	0.54	0.76
tyrosine-protein phosphatase non-receptor type substrate 1 precursor [Homo sapiens]	0.50	1.56	1.21	0.94	1.52
dihydrolipoyl dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	0.75	1.21	1.76	1.42	1.48
pre-mRNA-processing-splicing factor 8 [Homo sapiens]	0.62	0.95	0.67	0.77	0.89
mitogen-activated protein kinase 3 isoform 2 [Homo sapiens]	2.11	1.82	3.99	6.64	2.48
mitogen-activated protein kinase 3 isoform 1 [Homo sapiens]	2.11	1.82	3.99	6.64	2.48

coiled-coil domain-containing protein 57 [Homo sapiens]	2.58	0.70	2.07	2.51	2.60
myosin-11 isoform SM2B [Homo sapiens]	0.98	1.19	1.64	2.01	1.51
myosin-11 isoform SM1B [Homo sapiens]	0.98	1.19	1.64	2.01	1.51
arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform c [Homo sapiens]	0.21	0.79	1.81	3.81	1.29
actin-related protein 3B isoform 2 [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
ly6/PLAUR domain-containing protein 3 precursor [Homo sapiens]	2.38	0.71	0.49	0.27	0.92
core histone macro-H2A.1 isoform 3 [Homo sapiens]	0.66	0.98	0.89	0.64	0.76
ribose-5-phosphate isomerase [Homo sapiens]	2.34	0.94	0.73	0.55	0.70
hydroxyacylglutathione hydrolase, mitochondrial isoform 2 [Homo sapiens]	85.95	1.00	1.69	1.63	1.40
hydroxyacylglutathione hydrolase, mitochondrial isoform 1 precursor [Homo sapiens]	85.95	1.00	1.69	1.63	1.40
flotillin-2 [Homo sapiens]	0.23	0.93	0.31	0.26	0.44
vesicle-associated membrane protein-associated protein A isoform 1 [Homo sapiens]	0.77	0.94	1.40	1.71	0.89
vesicle-associated membrane protein-associated protein A isoform 2 [Homo sapiens]	0.77	0.94	1.40	1.71	0.89
2',3'-cyclic-nucleotide 3'-phosphodiesterase [Homo sapiens]	14.12	0.94	0.78	0.87	0.80
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform 1 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
low molecular weight phosphotyrosine protein phosphatase isoform d [Homo sapiens]	9.33	1.21	0.77	0.75	2.45
ras-related protein Rab-6B [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
ras-related protein Rab-24 [Homo sapiens]	0.41	0.77	0.34	0.27	0.51
neurocalcin-delta [Homo sapiens]	4.07	1.19	1.34	1.98	1.45
ATP-dependent RNA helicase A [Homo sapiens]	1.31	1.62	2.76	2.06	1.23
isochorismatase domain-containing protein 1 [Homo sapiens]	1.51	0.84	0.54	0.37	0.64
filamin-B isoform 2 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
apolipoprotein B-100 precursor [Homo sapiens]	0.46	0.61	0.40	0.35	0.43
coagulation factor V precursor [Homo sapiens]	1.37	0.75	0.35	0.24	0.54
neurofilament light polypeptide [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
histone H2A type 2-A [Homo sapiens]	2.38	1.39	0.57	0.34	0.67
glucose-6-phosphate 1-dehydrogenase isoform b [Homo sapiens]	0.91	1.19	1.46	2.10	1.24
60 kDa SS-A/Ro ribonucleoprotein isoform 1 [Homo sapiens]	0.66	1.42	1.86	1.51	1.54
coatamer subunit gamma-2 isoform 1 [Homo sapiens]	1.64	0.92	1.83	3.33	2.30
ubiquitin thioesterase OTUB1 [Homo sapiens]	1.61	0.79	0.91	0.85	0.79
alanine--tRNA ligase, cytoplasmic [Homo sapiens]	3.08	1.40	1.89	1.86	2.08
keratin, type II cytoskeletal 3 [Homo sapiens]	0.88	2.08	1.87	0.66	3.64
glucose-6-phosphate 1-dehydrogenase isoform a [Homo sapiens]	0.91	1.19	1.46	2.10	1.24
serine/threonine-protein kinase MST4 isoform 3 [Homo sapiens]	1.93	2.45	0.90	0.67	0.99
serine/threonine-protein kinase MST4 isoform 2 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
calpastatin isoform f [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
protein PML isoform 5 [Homo sapiens]	0.10	0.77	0.94	1.93	0.80
signal recognition particle subunit SRP72 isoform 1 [Homo sapiens]	0.45	0.78	0.56	0.64	0.65
galectin-7 [Homo sapiens]	1.31	0.34	0.30	0.11	0.37
WD40 repeat-containing protein SMU1 [Homo sapiens]	5.66	0.77	0.58	0.39	0.77
GPI mannosyltransferase 3 [Homo sapiens]	1.64	0.92	1.83	3.33	2.30

prosaposin isoform b preproprotein [Homo sapiens]	0.95	2.74	2.19	1.95	1.98
prosaposin isoform c preproprotein [Homo sapiens]	0.95	2.74	2.19	1.95	1.98
phospholipase B-like 1 precursor [Homo sapiens]	1.41	1.75	2.05	1.81	1.63
collagen alpha-1(I) chain preproprotein [Homo sapiens]	1.54	2.39	1.54	0.49	2.50
ribosome-binding protein 1 [Homo sapiens]	0.57	0.85	0.68	0.53	0.68
coagulation factor XIII B chain precursor [Homo sapiens]	0.62	0.64	0.40	0.24	0.50
kinesin light chain 1 isoform 2 [Homo sapiens]	0.83	0.71	0.48	0.43	0.63
CD177 antigen precursor [Homo sapiens]	0.67	4.54	2.31	1.41	3.22
ankyrin repeat and FYVE domain-containing protein 1 isoform 1 [Homo sapiens]	1.31	1.51	1.72	1.21	1.28
rho-related GTP-binding protein RhoC precursor [Homo sapiens]	1.68	0.93	0.76	0.75	0.93
dnaJ homolog subfamily C member 8 [Homo sapiens]	0.56	0.75	2.16	1.52	2.16
tyrosine-protein kinase Fgr [Homo sapiens]	0.75	1.30	2.49	2.22	1.00
spectrin beta chain, non-erythrocytic 1 isoform 1 [Homo sapiens]	1.18	1.24	1.27	1.56	1.26
spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	2.38	1.26	1.29	1.60	1.26
dnaJ homolog subfamily C member 13 [Homo sapiens]	2.66	0.85	1.21	1.81	1.48
gamma-interferon-inducible protein 16 isoform 2 [Homo sapiens]	0.35	0.64	0.33	0.30	0.44
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	5.61	1.30	0.79	1.20	1.18
tropomyosin alpha-3 chain isoform 1 [Homo sapiens]	1.34	1.21	1.91	5.18	1.71
tropomyosin alpha-3 chain isoform 4 [Homo sapiens]	1.31	1.62	0.90	0.89	0.92
tropomyosin alpha-3 chain isoform 3 [Homo sapiens]	0.91	1.90	0.88	2.17	0.92
tropomyosin alpha-3 chain isoform 5 [Homo sapiens]	1.31	1.62	0.90	0.89	0.92
keratin, type I cytoskeletal 28 [Homo sapiens]	0.80	0.91	0.18	0.12	0.40
E3 ubiquitin-protein ligase NEDD4 isoform 2 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4 isoform 1 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
protein S100-A7 [Homo sapiens]	5.04	0.94	1.65	0.58	10.37
spectrin alpha chain, erythrocytic 1 [Homo sapiens]	26.28	1.17	1.31	0.35	0.90
complement C3 precursor [Homo sapiens]	0.43	0.88	0.58	0.32	0.81
4-trimethylaminobutyaldehyde dehydrogenase [Homo sapiens]	1.57	1.18	0.78	0.56	0.74
receptor expression-enhancing protein 5 [Homo sapiens]	0.33	0.63	0.78	1.18	0.88
galectin-3 isoform 1 [Homo sapiens]	1.28	0.92	0.60	0.40	0.94
spectrin beta chain, non-erythrocytic 4 isoform sigma1 [Homo sapiens]	1.47	0.94	0.75	0.56	1.23
clathrin light chain A isoform c [Homo sapiens]	1.47	0.76	0.79	2.51	0.75
filamin-A isoform 1 [Homo sapiens]	0.95	1.73	1.24	1.56	1.19
ras GTPase-activating-like protein IQGAP2 isoform 1 [Homo sapiens]	1.18	1.30	1.54	1.57	0.96
septin-9 isoform c [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
myosin-14 isoform 2 [Homo sapiens]	0.95	1.96	1.65	1.97	1.70
WAS/WASL-interacting protein family member 1 [Homo sapiens]	0.64	1.19	1.72	0.95	1.17
apolipoprotein(a) precursor [Homo sapiens]	0.31	0.93	0.71	0.39	0.78
glycogen debranching enzyme isoform 1 [Homo sapiens]	1.37	1.30	0.96	0.92	0.81
glycogen debranching enzyme isoform 2 [Homo sapiens]	1.24	1.19	0.89	0.70	0.79
glycogen debranching enzyme isoform 3 [Homo sapiens]	1.24	1.19	0.89	0.70	0.79

filamin-C isoform a [Homo sapiens]	0.62	1.73	2.54	3.82	2.24
glycine--tRNA ligase precursor [Homo sapiens]	0.88	0.93	0.95	0.65	2.34
putative RNA-binding protein Luc7-like 2 isoform 1 [Homo sapiens]	0.45	0.77	0.63	0.52	0.58
polycystic kidney disease 2-like 2 protein isoform 1 [Homo sapiens]	0.19	0.61	0.39	0.20	0.67
3'(2'),5'-bisphosphate nucleotidase 1 isoform 1 [Homo sapiens]	2.54	0.93	1.24	1.17	1.21
ras-related protein Rab-6C [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
heterogeneous nuclear ribonucleoproteins C1/C2 isoform a [Homo sapiens]	0.88	2.45	1.63	4.80	1.51
heterogeneous nuclear ribonucleoproteins C1/C2 isoform b [Homo sapiens]	0.88	2.45	1.63	4.80	1.51
lysosomal Pro-X carboxypeptidase isoform 2 preproprotein [Homo sapiens]	2.54	1.17	1.26	0.73	0.94
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 [Homo sapiens]	1.37	0.69	0.75	1.40	0.78
leucine-rich repeat and coiled-coil domain-containing protein 1 [Homo sapiens]	3.70	1.75	1.98	2.19	2.11
AP-3 complex subunit delta-1 isoform 2 [Homo sapiens]	0.98	2.09	2.18	3.20	1.73
tumor necrosis factor alpha-induced protein 8 isoform a [Homo sapiens]	2.79	4.73	1.34	0.99	1.26
tumor necrosis factor alpha-induced protein 8 isoform b [Homo sapiens]	2.79	4.73	1.34	0.99	1.26
RAB6C-like [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
lactoylglutathione lyase [Homo sapiens]	14.64	0.98	1.18	2.25	1.23
complement factor H-related protein 1 precursor [Homo sapiens]	0.31	1.62	0.67	0.43	0.70
ribosomal L1 domain-containing protein 1 [Homo sapiens]		0.66	4.52	6.51	2.37
serine/arginine-rich splicing factor 1 isoform 2 [Homo sapiens]	0.69	1.24	0.66	0.29	0.82
extracellular superoxide dismutase [Cu-Zn] precursor [Homo sapiens]	2.15	2.46	0.50	0.27	0.57
ral GTPase-activating protein subunit alpha-2 [Homo sapiens]	149.10	0.78	1.21	0.31	1.24
heterogeneous nuclear ribonucleoprotein U-like protein 2 [Homo sapiens]	1.64	1.45	3.07	3.41	1.90
dmX-like protein 2 isoform 2 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
multifunctional protein ADE2 isoform 1 [Homo sapiens]	4.65	2.20	1.27	1.69	1.40
leukotriene-B(4) omega-hydroxylase 2 isoform a [Homo sapiens]	0.69	2.32	0.88	0.51	1.37
complement factor I preproprotein [Homo sapiens]	0.43	1.51	0.58	0.31	0.69
lysosomal protective protein isoform a precursor [Homo sapiens]	6.03	1.58	1.72	2.34	1.21
keratin, type II cytoskeletal 1 [Homo sapiens]	1.54	0.81	0.32	0.18	0.44
protein diaphanous homolog 1 isoform 1 [Homo sapiens]	1.21	0.93	1.43	2.51	2.30
protein diaphanous homolog 1 isoform 2 [Homo sapiens]	1.21	0.93	1.43	2.51	2.30
keratin, type II cytoskeletal 6B [Homo sapiens]	1.51	1.21	3.34	1.97	4.30
dihydropyrimidine dehydrogenase [NADP(+)] isoform 1 [Homo sapiens]	0.80	0.94	1.43	0.91	0.81
cation-independent mannose-6-phosphate receptor precursor [Homo sapiens]	1.34	1.27	2.47	0.78	1.54
acyl-CoA-binding protein isoform 3 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
acyl-CoA-binding protein isoform 2 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
WASH complex subunit strumpellin [Homo sapiens]	1.61	1.44	0.71	0.53	0.90
cullin-4B isoform 1 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
cullin-4B isoform 2 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83

rho GTPase-activating protein 9 isoform 1 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
rho GTPase-activating protein 9 isoform 3 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
rho GTPase-activating protein 9 isoform 2 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
protein-arginine deiminase type-2 [Homo sapiens]	0.75	0.85	0.71	1.44	2.39
protein-arginine deiminase type-3 [Homo sapiens]	0.88	0.82	0.50	0.87	0.96
transcription factor PU.1 isoform 2 [Homo sapiens]	1.64	1.19	0.80	3.82	0.87
transcription factor PU.1 isoform 1 [Homo sapiens]	1.64	1.19	0.80	3.82	0.87
BRO1 domain-containing protein BROX isoform a [Homo sapiens]	1.76	1.00	1.27	1.21	0.92
neutrophil defensin 1 precursor [Homo sapiens]	0.54	2.49	1.41	2.17	2.24
proliferation-associated protein 2G4 [Homo sapiens]	4.58	1.62	2.47	1.60	1.22
prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]	0.50	1.27	0.66	0.30	0.63
basement membrane-specific heparan sulfate proteoglycan core protein isoform b precursor [Homo sapiens]	1.37	4.07	2.56	0.83	3.52
DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]	1.41	0.94	0.80	1.00	0.97
serine/threonine-protein kinase 10 [Homo sapiens]	0.88	0.91	0.81	1.17	0.95
NADPH--cytochrome P450 reductase [Homo sapiens]	1.61	1.25	0.76	0.78	0.90
low affinity immunoglobulin gamma Fc region receptor III-B isoform 2 precursor [Homo sapiens]	0.54	2.08	2.56	1.18	4.26
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapiens]	0.67	1.25	0.79	0.43	2.16
transportin-1 isoform 1 [Homo sapiens]	2.38	0.68	1.23	2.81	1.48
FYVE, RhoGEF and PH domain-containing protein 3 isoform a [Homo sapiens]	0.88	0.89	1.22	1.52	0.78
CUGBP Elav-like family member 2 isoform 2 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
CUGBP Elav-like family member 2 isoform 4 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
neurabin-2 [Homo sapiens]	0.23	0.92	1.36	2.67	1.53
chitinase-3-like protein 1 precursor [Homo sapiens]	0.75	1.42	0.78	0.66	1.42
signal-regulatory protein beta-1 isoform 1 precursor [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
signal-regulatory protein beta-1 isoform 2 precursor [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
coagulation factor XII precursor [Homo sapiens]	0.26	0.62	0.34	0.21	0.52
probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 3 [Homo sapiens]	1.54	0.91	0.58	0.67	0.77
probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 4 [Homo sapiens]	1.54	0.91	0.58	0.67	0.77
D-dopachrome decarboxylase-like protein [Homo sapiens]	3.26	0.93	0.83	0.85	0.92
dedicator of cytokinesis protein 11 [Homo sapiens]	8.36	1.25	0.61	0.49	0.75
selenoprotein P isoform 1 precursor [Homo sapiens]	0.45	0.57	0.37	0.18	0.53
selenoprotein P isoform 2 [Homo sapiens]	0.45	0.57	0.37	0.18	0.53
thioredoxin reductase 1, cytoplasmic isoform 1 [Homo sapiens]	1.76	1.41	1.68	1.87	1.75
thioredoxin reductase 1, cytoplasmic isoform 3 [Homo sapiens]	1.76	1.41	1.68	1.87	1.75
septin-7 isoform 2 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
septin-7 isoform 1 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
heterogeneous nuclear ribonucleoprotein F [Homo sapiens]	1.21	1.38	1.24	1.46	1.24
DNA damage-binding protein 1 [Homo sapiens]	2.31	2.08	1.72	0.95	0.88
collagen alpha-1(IV) chain preproprotein [Homo sapiens]	1.28	0.76	0.56	0.69	0.76

sapiens]					
coatomer subunit alpha isoform 2 [Homo sapiens]	0.35	0.79	1.26	2.06	0.75
coatomer subunit alpha isoform 1 [Homo sapiens]	0.35	0.79	1.26	2.06	0.75
acetyl-CoA acetyltransferase, cytosolic [Homo sapiens]	15.35	0.91	1.55	1.48	1.38
beta-adrenergic receptor kinase 1 [Homo sapiens]	0.56	1.96	1.56	3.19	1.43
beta-adrenergic receptor kinase 2 [Homo sapiens]	0.33	1.37	3.35	8.99	2.08
probable ATP-dependent RNA helicase DDX17 isoform 3 [Homo sapiens]	2.38	1.30	0.93	1.98	0.70
serine-threonine kinase receptor-associated protein [Homo sapiens]	0.45	1.18	1.27	1.25	1.42
protein kinase C and casein kinase substrate in neurons protein 2 isoform A [Homo sapiens]	1.00	0.79	0.88	1.27	0.96
MOB kinase activator 1A [Homo sapiens]	1.71	0.96	1.29	1.44	0.94
poly(rC)-binding protein 2 isoform c [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
pro-interleukin-16 isoform 2 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
structural maintenance of chromosomes flexible hinge domain-containing protein 1 [Homo sapiens]	5.87	0.78	1.00	1.97	0.75
complement component receptor 1-like protein precursor [Homo sapiens]	1.31	1.90	0.69	0.38	0.68
xaa-Pro dipeptidase isoform 1 [Homo sapiens]	2.27	2.08	0.95	0.55	0.82
neurobeachin-like protein 2 [Homo sapiens]	1.64	0.74	0.56	0.64	0.61
signal recognition particle 14 kDa protein [Homo sapiens]	4.16	2.71	2.16	1.19	0.78
FK506-binding protein 15 [Homo sapiens]	1.64	1.21	0.94	0.98	1.54
ubiquitin-like modifier-activating enzyme 6 [Homo sapiens]	0.88	0.84	0.65	0.57	0.94
prothymosin alpha isoform 2 [Homo sapiens]	0.77	1.62	1.65	1.97	0.55
prothymosin alpha isoform 1 [Homo sapiens]	0.77	1.62	1.65	1.97	0.55
pre-mRNA-processing factor 40 homolog A [Homo sapiens]	0.33	0.92	1.46	2.49	1.57
myristoylated alanine-rich C-kinase substrate [Homo sapiens]	0.26	1.62	2.14	1.64	0.85
calcineurin-like phosphoesterase domain-containing protein 1 isoform a [Homo sapiens]	1.51	1.00	1.90	2.77	1.35
calcineurin-like phosphoesterase domain-containing protein 1 isoform b [Homo sapiens]	2.79	1.19	1.54	2.13	1.25
RNA-binding motif protein, X-linked-like-2 [Homo sapiens]	1.51	2.08	1.36	2.39	1.23
aldehyde dehydrogenase family 1 member A3 isoform 1 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
beta-2-glycoprotein 1 precursor [Homo sapiens]	0.25	0.76	0.40	0.20	0.54
keratin, type II cytoskeletal 75 [Homo sapiens]	1.34	2.59	0.88	0.69	1.48
POTE ankyrin domain family member F [Homo sapiens]	1.21	1.96	0.74	0.66	1.17
pleckstrin homology domain-containing family F member 1 [Homo sapiens]	1.21	2.37	5.64	5.87	2.46
eukaryotic translation initiation factor 3 subunit C-like protein [Homo sapiens]	2.15	1.34	1.75	1.78	1.37
eukaryotic translation initiation factor 5A-1-like [Homo sapiens]	9.42	0.77	1.31	1.66	1.23
heat shock protein HSP 90-alpha isoform 1 [Homo sapiens]	1.64	1.22	1.38	1.25	1.23
keratin, type I cytoskeletal 27 [Homo sapiens]	0.80	0.91	0.18	0.12	0.40
tenascin precursor [Homo sapiens]	1.54	4.13	0.95	0.61	1.42
dedicator of cytokinesis protein 10 DOCK10.1 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	1.64	1.22	1.38	1.25	1.23
IgGfC-binding protein precursor [Homo sapiens]	0.28	3.52	0.93	0.64	1.56
RNA-binding Raly-like protein isoform 1 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35

sapiens]					
RNA-binding Raly-like protein isoform 2 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35
spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
keratin, type II cytoskeletal 6C [Homo sapiens]	1.51	1.21	3.34	1.97	4.30
rho GTPase-activating protein 4 isoform 2 [Homo sapiens]	1.24	0.80	0.87	1.38	0.95
rap1 GTPase-activating protein 2 isoform 1 [Homo sapiens]	0.91	0.84	0.58	0.39	0.54
rap1 GTPase-activating protein 2 isoform 2 [Homo sapiens]	0.91	0.84	0.58	0.39	0.54
GMP reductase 1 [Homo sapiens]	5.11	0.97	1.48	1.45	2.39
inter-alpha-trypsin inhibitor heavy chain H1 isoform a precursor [Homo sapiens]	0.52	0.81	0.34	0.18	0.52
cytokine receptor-like factor 3 [Homo sapiens]	0.52	0.69	0.55	0.44	0.61
heterogeneous nuclear ribonucleoprotein R isoform 4 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
heterogeneous nuclear ribonucleoprotein R isoform 1 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
heterogeneous nuclear ribonucleoprotein R isoform 3 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
phosphatidylcholine transfer protein isoform 1 [Homo sapiens]	0.56	0.89	0.67	0.52	0.56
phosphatidylcholine transfer protein isoform 2 [Homo sapiens]	0.56	0.89	0.67	0.52	0.56
kininogen-1 isoform 1 precursor [Homo sapiens]	0.88	1.53	0.45	0.08	0.88
Y-box-binding protein 2 [Homo sapiens]	1.68	0.84	0.44	0.32	0.61
ubiquitin-fold modifier-conjugating enzyme 1 [Homo sapiens]	4.12	1.51	0.95	0.82	0.89
alpha-2-HS-glycoprotein preproprotein [Homo sapiens]	0.39	0.79	0.32	0.22	0.43
vesicle-fusing ATPase [Homo sapiens]	1.21	1.73	0.89	0.95	1.40
pleckstrin [Homo sapiens]	2.38	0.79	1.26	1.40	1.26
inosine-5'-monophosphate dehydrogenase 1 isoform c [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
N-acetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	0.35	0.68	0.29	0.16	0.44
zinc finger protein 836 [Homo sapiens]	2.00	1.54	1.82	1.86	1.63
protein-glutamine gamma-glutamyltransferase 4 [Homo sapiens]	0.14	0.70	0.32	0.22	3.48
tetranectin precursor [Homo sapiens]	0.56	0.78	0.29	0.18	0.32
26S proteasome non-ATPase regulatory subunit 8 [Homo sapiens]	1.93	1.62	1.23	1.33	1.48
proteasome subunit alpha type-4 isoform 2 [Homo sapiens]	4.84	1.34	1.80	1.44	1.43
purine nucleoside phosphorylase [Homo sapiens]	6.63	1.28	1.51	0.81	2.08
serine/threonine-protein kinase ATR [Homo sapiens]	0.56	0.91	0.43	0.20	0.78
bactericidal permeability-increasing protein precursor [Homo sapiens]	0.88	1.56	2.69	1.76	1.63
uncharacterized protein C9orf40 [Homo sapiens]	0.91	1.97	1.24	0.52	0.76
calpain-2 catalytic subunit isoform 1 [Homo sapiens]	1.71	0.94	0.71	0.44	0.74
heterogeneous nuclear ribonucleoprotein M isoform b [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
coronin-1C isoform a [Homo sapiens]	0.66	0.98	1.31	1.75	2.76
26S proteasome non-ATPase regulatory subunit 13 isoform 1 [Homo sapiens]	1.89	0.94	0.83	0.85	0.68
26S proteasome non-ATPase regulatory subunit 13 isoform 2 [Homo sapiens]	1.89	0.94	0.83	0.85	0.68
procollagen C-endopeptidase enhancer 1 precursor [Homo sapiens]	2.08	2.16	0.51	0.33	0.85
neurofilament medium polypeptide isoform 2 [Homo sapiens]	0.77	0.58	0.53	1.98	0.44

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neurofilament medium polypeptide isoform 1 [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
mitogen-activated protein kinase 3 isoform 3 [Homo sapiens]	2.11	1.82	3.99	6.64	2.48
puromycin-sensitive aminopeptidase [Homo sapiens]	2.38	0.83	0.85	1.00	0.81
filamin-A isoform 2 [Homo sapiens]	0.95	1.73	1.24	1.56	1.19
methyl-CpG-binding protein 2 isoform 2 [Homo sapiens]		0.42	1.87	1.00	1.65
ezrin [Homo sapiens]	1.34	1.62	1.39	1.64	1.23
tyrosine-protein kinase Lyn isoform B [Homo sapiens]	2.79	1.73	2.76	1.55	0.90
guanine nucleotide-binding protein G(o) subunit alpha isoform b [Homo sapiens]	2.00	1.19	2.02	2.08	1.34
pregnancy zone protein precursor [Homo sapiens]	0.57	0.88	0.44	0.25	0.75
neutrophil cytosol factor 4 isoform 2 [Homo sapiens]	2.00	0.78	0.92	1.40	0.84
ubiquitin-conjugating enzyme E2 K isoform 2 [Homo sapiens]	4.99	0.98	2.56	2.05	2.45
nascent polypeptide-associated complex subunit alpha isoform b [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
protein FAM65B isoform 1 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
septin-9 isoform a [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
septin-9 isoform b [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
septin-9 isoform e [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
septin-9 isoform d [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
proline-serine-threonine phosphatase-interacting protein 2 [Homo sapiens]	0.41	0.91	1.83	4.07	1.27
rho guanine nucleotide exchange factor 7 isoform c [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
rho guanine nucleotide exchange factor 7 isoform d [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
rho guanine nucleotide exchange factor 7 isoform a [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
complement component C8 gamma chain precursor [Homo sapiens]	0.83	0.98	0.52	0.30	0.62
osteoclast-stimulating factor 1 [Homo sapiens]	1.00	0.80	2.16	1.39	1.48
methylthioribulose-1-phosphate dehydratase [Homo sapiens]	0.91	1.57	2.01	2.15	2.76
cadherin-5 preproprotein [Homo sapiens]	0.39	0.79	0.27	0.11	0.40
dipeptidyl peptidase 1 isoform c precursor [Homo sapiens]	1.93	2.31	3.99	3.12	2.45
thyroid hormone receptor-associated protein 3 [Homo sapiens]	0.39	0.71	0.62	0.42	0.52
hematopoietic lineage cell-specific protein isoform 1 [Homo sapiens]	0.56	0.77	0.84	0.69	0.74
heat shock 70 kDa protein 1A/1B [Homo sapiens]	1.00	1.73	1.18	1.25	0.98
intercellular adhesion molecule 3 precursor [Homo sapiens]	1.28	1.44	1.54	0.62	1.63
plastin-2 [Homo sapiens]	0.67	1.30	1.77	1.86	1.47
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	0.77	2.50	1.34	0.78	1.65
pentraxin-related protein PTX3 precursor [Homo sapiens]	1.00	13.56	0.91	0.98	1.17
ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2 precursor [Homo sapiens]	0.66	1.98	1.27	0.96	1.23
coronin-7 isoform 1 [Homo sapiens]	0.39	0.77	0.64	0.70	0.84
cholesteryl ester transfer protein isoform 1 precursor [Homo sapiens]	0.25	0.53	0.40	0.23	0.77
rab GDP dissociation inhibitor beta isoform 2 [Homo sapiens]	2.76	1.31	1.65	1.45	1.58
lysosome-associated membrane glycoprotein 2 isoform C precursor [Homo sapiens]	0.83	1.77	1.61	0.92	1.88
protein XRP2 [Homo sapiens]	7.36	1.42	2.56	1.74	2.01

trypsin-3 isoform 1 preproprotein [Homo sapiens]	1.82	0.51	0.30	0.15	0.32
protein SET isoform 2 [Homo sapiens]	0.88	0.97	1.68	1.98	0.96
protein SET isoform 1 [Homo sapiens]	0.88	0.97	1.68	1.98	0.96
syntaxin-7 [Homo sapiens]	1.57	1.19	2.26	1.31	2.45
drebrin-like protein isoform c [Homo sapiens]	0.75	0.69	0.68	0.77	0.88
peptidyl-prolyl cis-trans isomerase A-like 4G [Homo sapiens]	4.58	1.90	2.68	2.49	1.93
complement C4-B preproprotein [Homo sapiens]	0.69	0.96	0.57	0.31	0.74
protein DJ-1 [Homo sapiens]	4.38	1.96	2.69	1.37	1.33
adenylosuccinate lyase isoform b [Homo sapiens]	3.52	0.88	0.58	0.56	0.70
serine/threonine-protein phosphatase 6 catalytic subunit isoform a [Homo sapiens]	2.08	1.40	0.84	1.52	0.80
serine/threonine-protein phosphatase 6 catalytic subunit isoform c [Homo sapiens]	2.08	1.40	0.84	1.52	0.80
haptoglobin isoform 2 preproprotein [Homo sapiens]	0.66	4.82	4.36	1.69	4.28
hepatoma-derived growth factor isoform b [Homo sapiens]	0.50	1.35	1.72	2.69	1.58
hepatoma-derived growth factor isoform c [Homo sapiens]	0.50	1.35	1.72	2.69	1.58
tripeptidyl-peptidase 2 [Homo sapiens]	4.31	2.71	1.34	1.39	1.23
tyrosine-protein kinase CSK [Homo sapiens]	1.21	0.83	0.69	0.73	0.75
versican core protein isoform 2 precursor [Homo sapiens]	1.34	6.39	0.70	0.49	1.81
arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 [Homo sapiens]	2.79	0.94	0.79	0.64	0.76
chromobox protein homolog 1 [Homo sapiens]	0.26	1.37	1.55	2.76	1.63
medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform b precursor [Homo sapiens]	1.21	1.26	0.98	0.66	0.83
N-myc-interactor [Homo sapiens]	0.28	0.85	0.84	0.73	0.85
rho GTPase-activating protein 15 [Homo sapiens]	1.18	2.45	1.72	2.14	1.28
serum amyloid A-2 protein isoform a precursor [Homo sapiens]	1.54	4.71	2.37	0.49	0.81
hexokinase-1 isoform HKI-td [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
hexokinase-1 isoform HKI [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
syntaxin-binding protein 2 isoform a [Homo sapiens]	1.44	0.98	1.58	2.21	1.28
syntaxin-binding protein 2 isoform b [Homo sapiens]	1.44	0.98	1.58	2.21	1.28
filamin-C isoform b [Homo sapiens]	0.62	1.73	2.54	3.82	2.24
acid ceramidase isoform b [Homo sapiens]	1.61	2.20	2.60	2.35	2.40
acid ceramidase isoform a preproprotein [Homo sapiens]	1.61	2.20	2.60	2.35	2.40
acid ceramidase isoform c [Homo sapiens]	1.61	2.20	2.60	2.35	2.40
nicotinamide riboside kinase 1 isoform 2 [Homo sapiens]	4.50	1.51	0.77	0.82	0.88
fructose-1,6-bisphosphatase 1 [Homo sapiens]	0.88	0.92	0.75	0.51	1.20
gelsolin isoform b [Homo sapiens]	7.53	2.39	0.77	0.78	1.82
low affinity immunoglobulin gamma Fc region receptor III-A isoform b precursor [Homo sapiens]	0.54	2.31	1.74	2.45	7.01
low affinity immunoglobulin gamma Fc region receptor III-A isoform c precursor [Homo sapiens]	0.54	2.31	1.74	2.45	7.01
low affinity immunoglobulin gamma Fc region receptor III-A isoform d precursor [Homo sapiens]	0.54	2.31	1.74	2.45	7.01
dipeptidyl peptidase 1 isoform a preproprotein [Homo sapiens]	1.37	2.13	2.47	2.37	2.07
delta-aminolevulinic acid dehydratase [Homo sapiens]	7.29	0.91	0.64	0.35	0.74
lysosomal protective protein isoform b precursor [Homo sapiens]	6.03	1.58	1.72	2.34	1.21
serine protease inhibitor Kazal-type 5 isoform a precursor [Homo sapiens]	5.15	2.08	0.69	0.49	1.42

serine protease inhibitor Kazal-type 5 isoform c precursor [Homo sapiens]	5.15	2.08	0.69	0.49	1.42
beta-hexosaminidase subunit alpha preproprotein [Homo sapiens]	0.57	0.64	0.56	0.41	0.50
proteoglycan 4 isoform B precursor [Homo sapiens]	0.77	1.73	0.65	0.40	0.78
proteoglycan 4 isoform C precursor [Homo sapiens]	0.54	2.32	0.70	0.41	0.79
proteoglycan 4 isoform D precursor [Homo sapiens]	0.77	1.73	0.65	0.40	0.78
72 kDa type IV collagenase isoform b [Homo sapiens]	1.51	4.10	0.89	0.56	0.82
KH domain-containing, RNA-binding, signal transduction-associated protein 2 [Homo sapiens]	0.45	1.25	2.57	3.85	1.93
complement component C6 precursor [Homo sapiens]	0.33	1.90	0.64	0.33	0.67
1,4-alpha-glucan-branching enzyme [Homo sapiens]	1.00	0.94	1.68	1.77	1.82
transferrin receptor protein 1 [Homo sapiens]	0.88	0.71	0.41	0.23	0.55
serine/threonine-protein kinase PAK 3 isoform b [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
serine/threonine-protein kinase PAK 3 isoform c [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
serine/threonine-protein kinase PAK 3 isoform d [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
PC4 and SFRS1-interacting protein isoform 1 [Homo sapiens]	0.67	1.22	2.79	4.74	1.52
PC4 and SFRS1-interacting protein isoform 2 [Homo sapiens]	0.67	1.22	2.79	4.74	1.52
SPARC-like protein 1 isoform 1 precursor [Homo sapiens]	0.11	5.08	1.77	1.00	1.73
ras-related protein Rab-11B [Homo sapiens]	1.64	1.94	1.31	1.35	1.53
serine/threonine-protein kinase PAK 1 isoform 1 [Homo sapiens]	0.39	0.76	0.39	0.24	0.68
carbonic anhydrase 1 isoform a [Homo sapiens]	66.88	0.88	0.96	0.30	2.08
vitamin K-dependent protein S preproprotein [Homo sapiens]	0.67	2.59	0.65	0.37	0.96
poly(rC)-binding protein 2 isoform d [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
poly(rC)-binding protein 2 isoform e [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
poly(rC)-binding protein 2 isoform f [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
poly(rC)-binding protein 2 isoform g [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
ubiquitin-like domain-containing CTD phosphatase 1 [Homo sapiens]	3.70	1.44	1.80	2.29	1.75
plasma serine protease inhibitor preproprotein [Homo sapiens]	0.39	0.48	0.25	0.13	0.42
phosphoribosyl pyrophosphate synthase-associated protein 1 [Homo sapiens]	3.17	1.26	1.45	1.43	0.84
hexokinase-3 [Homo sapiens]	0.57	0.91	0.97	1.19	0.92
alpha-actinin-1 isoform a [Homo sapiens]	0.80	1.62	1.34	1.65	1.81
alpha-actinin-1 isoform c [Homo sapiens]	0.80	1.62	1.38	1.74	1.81
elongation factor 1-delta isoform 2 [Homo sapiens]	0.25	0.83	0.71	0.44	0.67
elongation factor 1-delta isoform 4 [Homo sapiens]	3.61	0.87	0.98	0.90	2.68
lysine--tRNA ligase isoform 1 [Homo sapiens]	0.56	0.82	0.56	0.51	0.67
collagen type IV alpha-3-binding protein isoform 3 [Homo sapiens]	0.75	1.00	0.91	0.92	0.84
protein S100-A7-like 2 [Homo sapiens]	4.74	1.96	2.17	0.85	17.17
kinesin light chain 1 isoform 3 [Homo sapiens]	0.83	0.71	0.48	0.43	0.63
poly(rC)-binding protein 3 isoform 1 [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
poly(rC)-binding protein 3 isoform 2 [Homo sapiens]	1.64	0.82	2.47	5.20	1.96
SWI/SNF complex subunit SMARCC2 isoform c [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
signal recognition particle 9 kDa protein isoform 1 [Homo sapiens]	0.62	1.26	1.27	2.09	1.20
nicotinate phosphoribosyltransferase isoform 1 [Homo sapiens]	2.31	1.51	1.21	0.98	1.00

3-mercaptopyruvate sulfurtransferase isoform 1 [Homo sapiens]	9.20	0.73	0.64	0.66	0.74
latexin [Homo sapiens]	2.38	1.28	1.72	1.39	1.57
eukaryotic translation initiation factor 4E isoform 3 [Homo sapiens]	5.87	1.26	2.15	3.30	1.30
eukaryotic translation initiation factor 4E isoform 2 [Homo sapiens]	5.87	1.26	2.15	3.30	1.30
spectrin alpha chain, non-erythrocytic 1 isoform 1 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
high mobility group protein B2 [Homo sapiens]	0.35	0.97	0.93	2.27	1.39
serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 2 [Homo sapiens]	0.57	1.73	1.29	0.98	0.71
serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 3 [Homo sapiens]	0.57	1.73	1.29	0.98	0.71
26S protease regulatory subunit 10B [Homo sapiens]	3.26	0.65	0.76	0.97	0.62
calcium-binding protein 39 [Homo sapiens]	1.76	1.62	1.29	1.99	1.25
TFIIH basal transcription factor complex helicase XPD subunit isoform 2 [Homo sapiens]	0.28	1.39	3.23	4.06	2.56
keratin, type I cytoskeletal 10 [Homo sapiens]	2.38	0.78	0.45	0.18	0.56
thromboxane-A synthase isoform 1 [Homo sapiens]	0.39	0.66	0.33	0.20	0.53
thromboxane-A synthase isoform 2 [Homo sapiens]	0.39	0.66	0.33	0.20	0.53
dysferlin isoform 9 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 10 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 11 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 12 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 13 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 14 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 7 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 6 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 5 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 4 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 3 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
dysferlin isoform 1 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
hypoxia up-regulated protein 1 precursor [Homo sapiens]	0.67	1.63	1.92	1.39	1.94
dysferlin isoform 2 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
glial fibrillary acidic protein isoform 2 [Homo sapiens]	0.57	0.81	0.83	1.44	0.51
leucine-rich repeat flightless-interacting protein 2 isoform 3 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
cytosolic purine 5'-nucleotidase [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
copine-1 isoform b [Homo sapiens]	1.68	1.25	1.72	1.20	1.94
pseudouridine-5'-monophosphatase isoform b [Homo sapiens]	0.98	1.00	0.55	0.37	0.63
protein DEK isoform 2 [Homo sapiens]	0.77	2.45	0.82	0.98	1.23
syntaxin-16 isoform c [Homo sapiens]	4.35	2.32	0.51	0.30	0.45
syntaxin-16 isoform d [Homo sapiens]	4.35	2.32	0.51	0.30	0.45
phostensin [Homo sapiens]		4.42	2.21	2.10	7.30
pre-mRNA 3'-end-processing factor FIP1 isoform 2 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
pre-mRNA 3'-end-processing factor FIP1 isoform 3 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
hepatocyte growth factor-like protein precursor [Homo sapiens]	0.56	0.83	0.57	0.29	0.69
dynactin subunit 1 isoform 3 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
dynactin subunit 1 isoform 4 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
mitogen-activated protein kinase 9 isoform JNK2 gamma [Homo sapiens]	4.19	2.05	4.38	5.01	2.08

tyrosine-protein kinase SYK isoform Syk(S) [Homo sapiens]	0.39	0.81	1.52	3.16	0.97
thyroxine-binding globulin precursor [Homo sapiens]	0.46	1.51	0.46	0.28	0.68
protein-methionine sulfoxide oxidase MICAL1 isoform 1 [Homo sapiens]	0.67	1.19	2.29	1.74	1.88
arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform a [Homo sapiens]	0.21	0.79	1.81	3.81	1.29
arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform d [Homo sapiens]	0.21	0.79	1.81	3.81	1.29
arylacetamide deacetylase-like 2 precursor [Homo sapiens]	0.26	0.83	0.94	1.58	0.65
ARF GTPase-activating protein GIT2 isoform 4 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
ARF GTPase-activating protein GIT2 isoform 6 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
ARF GTPase-activating protein GIT2 isoform 5 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
L-lactate dehydrogenase A chain isoform 2 [Homo sapiens]	2.00	1.34	2.07	2.06	1.83
histone-binding protein RBBP4 isoform b [Homo sapiens]	0.52	2.20	1.22	0.85	0.88
histone-binding protein RBBP4 isoform c [Homo sapiens]	0.52	2.20	1.22	0.85	0.88
pseudouridine-5'-monophosphatase isoform a [Homo sapiens]	0.98	1.00	0.55	0.37	0.63
ras-related protein Rab-1A isoform 2 [Homo sapiens]	0.83	1.62	2.38	4.33	1.18
ubiquitin-40S ribosomal protein S27a precursor [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
protein phosphatase 1 regulatory subunit 21 isoform 1 [Homo sapiens]	2.27	1.38	3.90	0.69	0.61
interferon-induced, double-stranded RNA-activated protein kinase isoform a [Homo sapiens]	3.26	0.63	1.43	2.27	0.80
interferon-induced, double-stranded RNA-activated protein kinase isoform b [Homo sapiens]	3.26	0.63	1.43	2.27	0.80
polyadenylate-binding protein 4 isoform 1 [Homo sapiens]	0.77	2.32	1.47	1.65	1.39
polyadenylate-binding protein 4 isoform 3 [Homo sapiens]	0.77	2.32	1.47	1.65	1.39
mitochondrial peptide methionine sulfoxide reductase isoform b [Homo sapiens]	0.83	1.62	2.29	1.27	0.94
mitochondrial peptide methionine sulfoxide reductase isoform c [Homo sapiens]	0.83	1.90	2.29	1.27	0.94
dihydropteridine reductase [Homo sapiens]	1.41	1.26	2.49	2.17	0.96
target of Myb protein 1 isoform 3 [Homo sapiens]	0.88	2.08	0.76	0.78	0.89
target of Myb protein 1 isoform 4 [Homo sapiens]	0.43	0.95	0.73	0.71	0.83
target of Myb protein 1 isoform 2 [Homo sapiens]	0.88	2.08	0.76	0.78	0.89
signal-regulatory protein beta-1 isoform 3 precursor [Homo sapiens]	0.50	1.56	1.21	0.94	1.52
annexin A2 isoform 2 [Homo sapiens]	1.68	0.54	1.58	0.42	1.29
plastin-3 isoform 1 [Homo sapiens]	0.69	1.22	1.76	1.81	1.46
kallikrein-11 isoform 1 precursor [Homo sapiens]	2.15	0.54	0.23	0.15	0.41
periostin isoform 1 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
periostin isoform 2 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
periostin isoform 3 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
periostin isoform 4 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
dynamin-3 isoform b [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
UMP-CMP kinase isoform b [Homo sapiens]	4.99	0.80	0.91	1.47	0.82
protein RCC2 [Homo sapiens]	0.75	1.45	2.45	3.23	1.44
acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 2 [Homo sapiens]	2.79	0.78	0.64	0.98	0.33
acidic leucine-rich nuclear phosphoprotein 32 family	0.95	0.80	0.83	1.97	0.90

member E isoform 3 [Homo sapiens]					
apolipoprotein L1 isoform c [Homo sapiens]	0.56	0.67	0.37	0.22	0.41
leucine-rich repeat flightless-interacting protein 1 isoform 4 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
leucine-rich repeat flightless-interacting protein 1 isoform 1 [Homo sapiens]	3.70	2.59	0.75	0.57	0.88
leucine-rich repeat flightless-interacting protein 1 isoform 2 [Homo sapiens]	0.66	2.59	1.55	2.39	1.37
leucine-rich repeat flightless-interacting protein 1 isoform 3 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
leucine-rich repeat flightless-interacting protein 1 isoform 5 [Homo sapiens]	0.57	1.62	1.21	2.51	0.74
interleukin enhancer-binding factor 3 isoform d [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
interleukin enhancer-binding factor 3 isoform e [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
B-cell receptor-associated protein 31 isoform a [Homo sapiens]	1.64	1.44	1.37	2.34	1.54
coatamer subunit delta isoform 2 [Homo sapiens]	0.33	2.59	1.93	2.25	1.50
serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform a [Homo sapiens]	0.77	0.82	0.62	0.55	0.68
serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform c [Homo sapiens]	0.77	0.82	0.62	0.55	0.68
ankyrin-1 isoform 9 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
probable ATP-dependent RNA helicase DDX4 isoform 2 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
protein-arginine deiminase type-4 [Homo sapiens]	1.34	0.91	0.64	1.38	1.17
inosine-5'-monophosphate dehydrogenase 1 isoform e [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
inosine-5'-monophosphate dehydrogenase 1 isoform f [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
inosine-5'-monophosphate dehydrogenase 1 isoform g [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
inosine-5'-monophosphate dehydrogenase 1 isoform d [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
capZ-interacting protein [Homo sapiens]	0.19	0.70	1.19	1.28	0.76
116 kDa U5 small nuclear ribonucleoprotein component isoform b [Homo sapiens]	1.31	0.73	0.65	0.67	0.70
glyoxalase domain-containing protein 4 [Homo sapiens]	5.87	1.62	1.31	1.26	1.88
activated RNA polymerase II transcriptional coactivator p15 [Homo sapiens]	0.57	1.25	0.61	0.67	1.23
caskin-2 isoform a [Homo sapiens]	0.64	2.59	1.39	1.51	2.39
caskin-2 isoform b [Homo sapiens]	0.64	2.59	1.39	1.51	2.39
apoptosis inhibitor 5 isoform a [Homo sapiens]	0.50	0.85	0.70	0.69	0.79
apoptosis inhibitor 5 isoform c [Homo sapiens]	0.50	0.85	0.70	0.69	0.79
eukaryotic translation initiation factor 5A-1 isoform A [Homo sapiens]	10.46	0.78	1.43	1.86	1.30
plasminogen activator inhibitor 2 [Homo sapiens]	0.56	2.26	2.83	0.92	2.35
partner of Y14 and mago isoform 2 [Homo sapiens]	0.80	1.87	0.93	1.81	1.46
peptidyl-prolyl cis-trans isomerase A-like 4A/B/C [Homo sapiens]	4.55	1.80	2.16	2.33	1.87
protein phosphatase 1 regulatory subunit 12A isoform b [Homo sapiens]	0.43	0.91	0.91	1.38	1.81
tyrosine-protein kinase Fes/Fps isoform 4 [Homo sapiens]	2.33	2.59	0.81	0.51	0.92
COP9 signalosome complex subunit 2 isoform 2 [Homo sapiens]	5.66	0.92	1.37	1.59	1.17
cysteine and histidine-rich domain-containing protein 1 isoform a [Homo sapiens]	2.38	0.97	2.33	3.68	1.29
cysteine and histidine-rich domain-containing protein 1 isoform b [Homo sapiens]	2.38	0.97	2.33	3.68	1.29

extracellular matrix protein 1 isoform 1 precursor [Homo sapiens]	1.18	0.99	0.44	0.23	0.62
extracellular matrix protein 1 isoform 2 precursor [Homo sapiens]	0.91	0.99	0.41	0.19	0.56
coatamer subunit beta [Homo sapiens]	1.31	0.95	2.69	1.89	1.23
maltase-glucoamylase, intestinal [Homo sapiens]	21.72	0.93	0.54	0.35	0.58
proteasome subunit alpha type-1 isoform 3 [Homo sapiens]	3.56	1.62	2.72	2.59	2.10
docking protein 3 isoform 1 [Homo sapiens]	1.34	0.89	0.67	0.89	0.75
inositol monophosphatase 1 isoform 2 [Homo sapiens]	1.18	1.21	1.60	1.51	1.57
inositol monophosphatase 1 isoform 3 [Homo sapiens]	1.51	1.30	1.46	1.63	1.43
C-1-tetrahydrofolate synthase, cytoplasmic [Homo sapiens]	2.00	1.90	2.09	1.77	0.98
D-dopachrome decarboxylase related protein [Homo sapiens]	1.96	0.88	0.61	0.51	0.90
ubiquitin-like modifier-activating enzyme ATG7 isoform b [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
ubiquitin-like modifier-activating enzyme ATG7 isoform c [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
proteasome subunit beta type-5 isoform 3 [Homo sapiens]	4.50	1.90	0.76	0.45	2.68
myosin regulatory light chain 12B [Homo sapiens]	0.91	0.87	1.60	1.19	0.98
E3 ubiquitin-protein ligase NEDD4-like isoform 1 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4-like isoform 4 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4-like isoform 5 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4-like isoform 6 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
poly(rC)-binding protein 1 [Homo sapiens]	0.80	0.77	0.98	1.43	1.29
E3 ubiquitin-protein ligase NEDD4-like isoform 2 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
talin-1 [Homo sapiens]	1.21	0.97	1.21	1.51	2.08
echinoderm microtubule-associated protein-like 4 isoform b [Homo sapiens]	1.28	1.28	1.43	1.30	1.25
calmodulin-like protein 5 [Homo sapiens]	8.60	2.59	1.51	0.45	5.50
tropomyosin alpha-4 chain isoform 1 [Homo sapiens]	3.70	0.73	1.21	0.62	0.97
pantetheinase precursor [Homo sapiens]	0.16	0.77	0.41	0.33	0.56
regulator complex protein LAMTOR2 isoform 2 [Homo sapiens]	0.50	1.53	1.83	2.24	1.42
RNA-binding motif protein, X-linked-like-3 [Homo sapiens]	1.76	0.92	1.26	2.22	2.76
aldehyde dehydrogenase family 16 member A1 isoform 1 [Homo sapiens]	6.30	1.25	1.27	1.33	2.53
aldehyde dehydrogenase family 16 member A1 isoform 2 [Homo sapiens]	6.30	1.25	1.27	1.33	2.53
non-POU domain-containing octamer-binding protein isoform 1 [Homo sapiens]	0.77	2.08	0.74	0.83	1.29
non-POU domain-containing octamer-binding protein isoform 2 [Homo sapiens]	0.77	2.08	0.74	0.83	1.29
stathmin isoform b [Homo sapiens]	0.88	0.88	1.36	1.73	0.84
thioredoxin domain-containing protein 5 isoform 3 [Homo sapiens]	1.00	1.62	1.47	1.70	1.30
Y-box-binding protein 3 isoform a [Homo sapiens]	1.68	0.84	0.44	0.32	0.61
Y-box-binding protein 3 isoform b [Homo sapiens]	1.68	0.84	0.44	0.32	0.61
uncharacterized protein KIAA0825 isoform 1 [Homo sapiens]	0.35	0.69	0.31	0.18	0.49
peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]	0.77	2.08	1.78	1.63	0.85
peptidyl-prolyl cis-trans isomerase FKBP5 isoform 2 [Homo sapiens]	0.91	0.99	0.85	0.61	0.65

integrin alpha-M isoform 1 precursor [Homo sapiens]	1.24	1.51	0.98	0.49	0.92
myosin-14 isoform 3 [Homo sapiens]	0.95	1.96	1.65	1.97	1.70
interstitial collagenase isoform 2 [Homo sapiens]	1.31	6.74	1.44	0.71	1.90
platelet-activating factor acetylhydrolase IB subunit gamma [Homo sapiens]	10.65	0.64	0.64	0.37	0.63
complement C2 isoform 2 precursor [Homo sapiens]	0.39	1.96	0.71	0.32	0.67
insulin-like growth factor-binding protein complex acid labile subunit isoform 1 precursor [Homo sapiens]	0.62	0.54	0.25	0.13	0.27
calpain-2 catalytic subunit isoform 2 [Homo sapiens]	1.71	0.94	0.71	0.44	0.74
prostaglandin reductase 1 isoform 2 [Homo sapiens]	1.21	0.97	1.26	1.69	1.63
prostaglandin reductase 1 isoform 1 [Homo sapiens]	1.21	0.97	1.26	1.69	1.63
triosephosphate isomerase isoform 2 [Homo sapiens]	2.02	1.21	1.43	1.25	1.39
protein-methionine sulfoxide oxidase MICAL1 isoform 2 [Homo sapiens]	0.14	1.34	1.79	4.64	1.26
protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 1 [Homo sapiens]	4.35	2.08	1.24	1.36	2.39
heterogeneous nuclear ribonucleoprotein Q isoform 1 [Homo sapiens]	3.86	0.91	1.54	1.29	0.91
heterogeneous nuclear ribonucleoprotein Q isoform 4 [Homo sapiens]	3.86	0.91	1.54	1.29	0.91
heterogeneous nuclear ribonucleoprotein Q isoform 2 [Homo sapiens]	3.86	0.70	1.54	1.29	0.81
heterogeneous nuclear ribonucleoprotein Q isoform 3 [Homo sapiens]	4.58	0.80	0.87	0.94	0.90
heterogeneous nuclear ribonucleoprotein Q isoform 6 [Homo sapiens]	4.58	0.80	0.87	0.94	0.90
epidermal growth factor receptor substrate 15 isoform B [Homo sapiens]	0.62	1.40	1.37	1.35	0.88
small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens]	1.96	1.31	1.87	0.40	0.76
dihydropyrimidine dehydrogenase [NADP(+)] isoform 2 [Homo sapiens]	0.80	0.94	1.43	0.91	0.81
polyamine-modulated factor 1-binding protein 1 isoform a [Homo sapiens]	1.57	1.45	1.37	2.24	1.58
polyamine-modulated factor 1-binding protein 1 isoform b [Homo sapiens]	1.57	1.45	1.37	2.24	1.58
dedicator of cytokinesis protein 8 isoform 1 [Homo sapiens]		1.38	2.33	3.23	2.44
histone H2B type 2-F isoform b [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
THO complex subunit 4 [Homo sapiens]	0.77	1.26	1.28	2.09	1.36
delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial isoform b [Homo sapiens]	0.69	1.31	0.67	0.37	0.80
glycogen [starch] synthase, muscle isoform 2 [Homo sapiens]	0.54	2.08	0.89	0.67	0.83
leucine-rich repeat-containing protein 17 isoform 2 precursor [Homo sapiens]	0.11	0.75	0.24	0.14	0.39
collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]	2.11	1.59	0.52	0.32	0.82
collagen alpha-3(VI) chain isoform 3 precursor [Homo sapiens]	2.19	0.98	0.45	0.22	0.70
collagen alpha-3(VI) chain isoform 2 precursor [Homo sapiens]	2.19	0.98	0.45	0.22	0.70
programmed cell death 6-interacting protein isoform 2 [Homo sapiens]	1.82	0.80	1.54	2.51	0.77
RNA binding motif protein, X-linked-like-1 [Homo sapiens]	1.71	0.92	1.26	2.22	2.76
clathrin heavy chain 2 isoform 1 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
clathrin heavy chain 2 isoform 2 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
rho guanine nucleotide exchange factor 2 isoform 1 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
rho guanine nucleotide exchange factor 2 isoform 2 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
RNA-binding protein EWS isoform 1 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52

RNA-binding protein EWS isoform 3 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
RNA-binding protein EWS isoform 4 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
TPT1-like protein [Homo sapiens]	2.02	1.25	3.23	3.95	1.94
polypyrimidine tract-binding protein 3 isoform 3 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
glycogen phosphorylase, liver form isoform 2 [Homo sapiens]	0.67	0.91	1.51	1.30	1.39
versican core protein isoform 3 precursor [Homo sapiens]	1.18	6.12	0.70	0.42	0.92
versican core protein isoform 4 precursor [Homo sapiens]	1.34	6.39	0.70	0.49	1.81
perilipin-3 isoform 1 [Homo sapiens]	1.54	0.82	0.76	0.66	0.79
perilipin-3 isoform 2 [Homo sapiens]	1.54	0.82	0.76	0.66	0.79
perilipin-3 isoform 3 [Homo sapiens]	1.54	0.82	0.76	0.66	0.79
peptidyl-prolyl cis-trans isomerase A-like 4D [Homo sapiens]	4.58	1.90	2.68	2.49	1.93
ras-related protein Rab-10 [Homo sapiens]	2.38	2.45	1.21	1.25	0.99
filamin-B isoform 1 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
filamin-B isoform 3 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
filamin-B isoform 4 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
actin-related protein 3C precursor [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
disintegrin and metalloproteinase domain-containing protein 8 isoform 1 precursor [Homo sapiens]	1.37	2.71	2.06	6.93	1.63
disintegrin and metalloproteinase domain-containing protein 8 isoform 3 precursor [Homo sapiens]	1.37	2.71	2.06	6.93	1.63
glycogen phosphorylase, muscle form isoform 2 [Homo sapiens]	1.68	0.79	1.36	0.92	2.30
rho GTPase-activating protein 4 isoform 1 [Homo sapiens]	1.24	0.80	0.87	1.38	0.95
RNA-binding motif protein, X chromosome isoform 2 [Homo sapiens]	1.51	2.08	1.36	2.39	1.23
nuclear factor NF-kappa-B p105 subunit isoform 2 [Homo sapiens]	1.96	0.55	0.40	0.24	0.44
alpha-2-antiplasmin isoform a precursor [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
alpha-2-antiplasmin isoform b precursor [Homo sapiens]	0.66	0.91	0.51	0.29	0.68
L-lactate dehydrogenase A chain isoform 3 [Homo sapiens]	0.88	1.35	2.05	2.13	1.87
L-lactate dehydrogenase A chain isoform 4 [Homo sapiens]	0.88	1.41	2.19	2.17	2.01
L-lactate dehydrogenase A chain isoform 5 [Homo sapiens]	0.88	1.41	2.19	2.17	2.01
protein 4.1 isoform 1 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
protein 4.1 isoform 3 [Homo sapiens]	24.91	0.94	0.88	0.46	0.92
protein 4.1 isoform 5 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
AP-1 complex subunit beta-1 isoform b [Homo sapiens]	1.41	2.08	1.31	1.30	1.25
AP-1 complex subunit beta-1 isoform a [Homo sapiens]	1.41	2.08	1.31	1.30	1.25
AP-1 complex subunit beta-1 isoform c [Homo sapiens]	1.41	1.51	1.21	1.31	2.16
suprabasin isoform 1 precursor [Homo sapiens]	0.66	0.93	2.26	0.56	1.38
xaa-Pro dipeptidase isoform 2 [Homo sapiens]	2.27	2.08	0.95	0.55	0.82
tropomodulin-1 [Homo sapiens]	3.90	2.08	1.27	1.52	2.16
thromboxane-A synthase isoform 3 [Homo sapiens]	0.39	0.66	0.33	0.20	0.53
thromboxane-A synthase isoform 4 [Homo sapiens]	0.39	0.66	0.33	0.20	0.53
T-complex protein 1 subunit eta isoform c [Homo sapiens]	2.19	1.25	1.54	1.19	0.93
T-complex protein 1 subunit eta isoform d [Homo sapiens]	2.19	1.25	1.54	1.19	0.93

sapiens]					
rho GTPase-activating protein 25 isoform a [Homo sapiens]	0.64	1.00	1.43	0.98	0.94
rho GTPase-activating protein 25 isoform c [Homo sapiens]	0.64	1.00	1.43	0.98	0.94
rho GTPase-activating protein 25 isoform d [Homo sapiens]	0.56	0.95	1.23	1.74	1.21
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 2 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
inter-alpha-trypsin inhibitor heavy chain H1 isoform b [Homo sapiens]	0.45	0.85	0.33	0.18	0.52
inter-alpha-trypsin inhibitor heavy chain H1 isoform c [Homo sapiens]	0.56	0.87	0.34	0.19	0.54
inter-alpha-trypsin inhibitor heavy chain H4 isoform 2 precursor [Homo sapiens]		0.88	0.41	0.04	0.28
kininogen-1 isoform 3 precursor [Homo sapiens]	0.19	0.54	0.28	0.08	0.30
coiled-coil domain-containing protein 88B precursor [Homo sapiens]	0.33	1.90	1.68	1.66	0.76
probable ATP-dependent RNA helicase DDX4 isoform 4 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
L-selectin precursor [Homo sapiens]	0.41	1.96	0.46	0.32	0.61
complement factor H-related protein 3 isoform 2 precursor [Homo sapiens]	0.33	1.38	0.90	0.53	0.94
probable ATP-dependent RNA helicase DDX4 isoform 3 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
cystatin-F precursor [Homo sapiens]	0.64	0.77	0.27	0.22	0.43
lysosomal protective protein isoform c precursor [Homo sapiens]	6.03	1.58	1.72	2.34	1.21
kallikrein-11 isoform 3 precursor [Homo sapiens]	2.15	0.54	0.23	0.15	0.41
xaa-Pro aminopeptidase 1 isoform 1 [Homo sapiens]	1.00	0.91	1.18	1.65	0.93
xaa-Pro aminopeptidase 1 isoform 2 [Homo sapiens]	1.00	0.91	1.18	1.65	0.93
protein phosphatase 1 regulatory subunit 12B isoform a [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
beta-glucuronidase isoform 1 precursor [Homo sapiens]	0.75	1.82	1.64	0.96	2.76
phospholysine phosphohistidine inorganic pyrophosphate phosphatase isoform 1 [Homo sapiens]	1.00	0.70	0.40	0.24	0.50
plasminogen isoform 2 precursor [Homo sapiens]	0.14	0.37	0.30	0.10	0.63
NAD-dependent malic enzyme, mitochondrial isoform 2 precursor [Homo sapiens]	0.67	2.59	0.99	0.85	0.93
cytosolic non-specific dipeptidase isoform 2 [Homo sapiens]	2.33	0.87	1.43	0.49	0.97
spermatid perinuclear RNA-binding protein isoform 2 [Homo sapiens]	0.69	1.25	1.20	1.29	1.48
N(4)-(beta-N-acetylglucosaminy)-L-asparaginase isoform 1 preproprotein [Homo sapiens]	0.31	2.08	0.88	0.75	1.29
N(4)-(beta-N-acetylglucosaminy)-L-asparaginase isoform 2 preproprotein [Homo sapiens]	0.31	2.08	0.88	0.75	1.29
tyrosine-protein kinase HCK isoform c [Homo sapiens]	1.21	0.93	1.54	1.00	0.84
tyrosine-protein kinase HCK isoform d [Homo sapiens]	1.21	0.93	1.54	1.00	0.84
tyrosine-protein kinase HCK isoform e [Homo sapiens]	1.21	0.93	1.54	1.00	0.84
tyrosine-protein kinase HCK isoform b [Homo sapiens]	1.21	0.93	1.54	1.00	0.84
plastin-1 [Homo sapiens]	0.26	2.08	0.94	0.94	1.23
plastin-3 isoform 2 [Homo sapiens]	0.69	1.22	1.76	1.81	1.46
pro-interleukin-16 isoform 3 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
AMP deaminase 3 isoform 1B [Homo sapiens]	1.44	0.85	0.80	0.83	0.81
AMP deaminase 3 isoform 4 [Homo sapiens]	1.51	0.84	0.80	0.90	0.96
leukocyte immunoglobulin-like receptor subfamily A member 3 isoform 1 precursor [Homo sapiens]	0.57	1.25	0.90	1.97	1.57
leukocyte immunoglobulin-like receptor subfamily A member 3 isoform 2 precursor [Homo sapiens]	0.57	1.25	0.90	1.97	1.57

complement C1r subcomponent-like protein isoform 1 precursor [Homo sapiens]	0.80	0.91	0.56	0.30	0.53
phosphoglucomutase-1 isoform 2 [Homo sapiens]	0.91	0.95	2.49	1.59	0.99
phosphoglucomutase-1 isoform 3 [Homo sapiens]	1.31	0.89	1.37	1.59	0.83
lysosomal alpha-mannosidase isoform 2 precursor [Homo sapiens]	3.61	1.79	1.26	0.66	1.35
60 kDa SS-A/Ro ribonucleoprotein isoform 3 [Homo sapiens]	0.66	1.42	1.86	1.51	1.54
60 kDa SS-A/Ro ribonucleoprotein isoform 4 [Homo sapiens]	0.66	1.42	1.86	1.51	1.54
nebulette isoform 3 [Homo sapiens]	0.54	0.87	1.21	0.89	1.61
L-lactate dehydrogenase B chain [Homo sapiens]	4.02	1.24	1.91	1.58	1.63
monocyte differentiation antigen CD14 precursor [Homo sapiens]	0.57	1.95	0.70	0.39	0.61
dmX-like protein 2 isoform 1 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
dmX-like protein 2 isoform 3 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
tyrosine-protein kinase SYK isoform Syk(L) [Homo sapiens]	0.39	0.81	1.52	3.16	0.97
galectin-3 isoform 2 [Homo sapiens]	2.38	1.64	1.18	0.77	1.69
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform c [Homo sapiens]	1.96	0.94	1.23	1.94	0.98
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform d [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform e [Homo sapiens]	3.39	0.78	0.78	0.75	0.88
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform isoform 2 [Homo sapiens]	1.64	0.89	2.26	1.51	0.99
hyaluronan-binding protein 2 isoform 2 [Homo sapiens]	0.33	0.74	0.33	0.22	0.53
adiponectin precursor [Homo sapiens]	0.57	2.52	1.72	0.68	2.35
signal recognition particle receptor subunit alpha isoform 2 [Homo sapiens]	0.91	1.44	1.39	1.27	1.18
serum amyloid A-1 protein preproprotein [Homo sapiens]	1.93	3.38	1.64	0.52	0.65
syntaxin-3 isoform 2 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
acyl-CoA-binding protein isoform 5 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
acyl-CoA-binding protein isoform 6 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
N-acetyl-D-glucosamine kinase [Homo sapiens]	0.75	0.94	1.21	1.40	1.34
acyl-CoA-binding protein isoform 4 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
complement C2 isoform 3 [Homo sapiens]	0.39	1.96	0.71	0.32	0.67
immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]	0.31	0.76	0.34	0.18	0.70
abl interactor 1 isoform e [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform f [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform g [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform h [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform i [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform j [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform k [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
abl interactor 1 isoform l [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
pseudouridine-5'-monophosphatase isoform d [Homo sapiens]	0.98	1.00	0.55	0.37	0.63
glycogenin-1 isoform 2 [Homo sapiens]	1.31	1.31	1.54	1.89	1.40
glycogenin-1 isoform 3 [Homo sapiens]	1.31	1.71	2.30	1.68	1.61

glucose-6-phosphate isomerase isoform 1 [Homo sapiens]	0.80	1.27	1.62	1.45	1.44
fibrinogen beta chain isoform 2 preproprotein [Homo sapiens]	1.64	1.96	1.46	1.25	3.76
platelet-activating factor acetylhydrolase IB subunit beta isoform b [Homo sapiens]	2.00	0.62	0.58	0.67	0.61
platelet-activating factor acetylhydrolase IB subunit beta isoform c [Homo sapiens]	2.00	0.62	0.58	0.67	0.61
platelet-activating factor acetylhydrolase IB subunit beta isoform d [Homo sapiens]	2.00	0.62	0.58	0.67	0.61
clathrin light chain A isoform d [Homo sapiens]	1.47	0.76	0.79	2.51	0.75
clathrin light chain A isoform f [Homo sapiens]	1.47	0.76	0.79	2.51	0.75
clathrin light chain A isoform e [Homo sapiens]	0.57	0.85	0.66	0.57	0.77
hydroxyacyl-coenzyme A dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	0.64	1.53	1.96	0.58	0.88
hydroxyacyl-coenzyme A dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]	0.64	1.53	1.96	0.58	0.88
ES1 protein homolog, mitochondrial isoform 1a precursor [Homo sapiens]	0.46	0.81	0.94	0.42	0.76
SH3 domain-containing kinase-binding protein 1 isoform c [Homo sapiens]	0.88	0.91	0.95	1.39	1.54
WD repeat-containing protein 44 isoform 2 [Homo sapiens]	0.77	0.83	0.58	0.44	0.58
WD repeat-containing protein 44 isoform 3 [Homo sapiens]	0.77	0.83	0.58	0.44	0.58
nck-associated protein 1-like isoform 2 [Homo sapiens]	9.83	1.74	0.76	0.80	1.45
rho GDP-dissociation inhibitor 1 isoform b [Homo sapiens]	1.37	0.96	1.62	2.11	1.21
nitrilase homolog 1 isoform 2 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
nitrilase homolog 1 isoform 3 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
dedicator of cytokinesis protein 8 isoform 2 [Homo sapiens]		1.38	2.33	3.23	2.44
dynammin-2 isoform 5 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
neutrophil cytosol factor 2 isoform 3 [Homo sapiens]	0.69	0.71	0.75	2.25	0.84
neutrophil cytosol factor 2 isoform 2 [Homo sapiens]	0.69	0.71	0.75	2.25	0.84
dynactin subunit 1 isoform 5 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
dynactin subunit 1 isoform 6 [Homo sapiens]	1.21	1.51	1.36	1.69	1.23
cysteine-rich secretory protein 3 isoform 1 precursor [Homo sapiens]	0.31	1.18	0.56	0.61	1.21
cysteine-rich secretory protein 3 isoform 2 precursor [Homo sapiens]	0.31	1.18	0.56	0.61	1.21
protein canopy homolog 2 isoform 2 precursor [Homo sapiens]	7.48	1.30	1.75	1.35	2.53
actin-related protein 2/3 complex subunit 1A isoform 2 [Homo sapiens]	1.18	1.34	1.90	2.41	1.39
glutathione S-transferase omega-1 isoform 2 [Homo sapiens]	2.83	1.24	1.61	1.64	1.34
glutathione S-transferase omega-1 isoform 3 [Homo sapiens]	3.26	1.24	1.61	1.78	1.34
26S proteasome non-ATPase regulatory subunit 1 isoform 2 [Homo sapiens]	0.54	2.08	0.76	0.67	0.68
echinoderm microtubule-associated protein-like 2 isoform 1 [Homo sapiens]	0.56	1.34	0.69	0.69	1.23
echinoderm microtubule-associated protein-like 2 isoform 3 [Homo sapiens]	0.56	1.34	0.69	0.69	1.23
coronin-1A [Homo sapiens]	0.43	0.99	1.38	1.87	1.29
transportin-3 isoform 2 [Homo sapiens]	20.10	0.63	0.30	0.25	0.25
serine/threonine-protein phosphatase 2A activator isoform e [Homo sapiens]	9.83	1.00	1.18	1.25	0.89
ATP-dependent RNA helicase DDX3X isoform 2 [Homo sapiens]	0.83	0.77	0.92	1.62	0.92
ATP-dependent RNA helicase DDX3X isoform 3 [Homo sapiens]	0.83	0.77	0.92	1.62	0.92

protein phosphatase 1 regulatory subunit 21 isoform 5 [Homo sapiens]	2.27	1.38	3.90	0.69	0.61
T-complex protein 1 subunit zeta-2 isoform 2 [Homo sapiens]	2.79	0.97	2.29	1.57	1.63
T-complex protein 1 subunit zeta-2 isoform 3 [Homo sapiens]	2.79	0.97	2.29	1.57	1.63
annexin A6 isoform 2 [Homo sapiens]	0.91	1.89	1.69	1.79	1.63
dedicator of cytokinesis protein 8 isoform 3 [Homo sapiens]		1.38	2.33	3.23	2.44
cysteine and glycine-rich protein 1 isoform 3 [Homo sapiens]	1.44	1.73	0.82	0.95	0.93
cysteine and glycine-rich protein 1 isoform 1 [Homo sapiens]	1.44	1.73	0.82	0.95	0.93
PML-RARA-regulated adapter molecule 1 [Homo sapiens]	0.33	0.82	1.52	2.49	1.74
protein crumbs homolog 1 isoform 2 precursor [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
eukaryotic translation initiation factor 4 gamma 1 isoform 1 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
eukaryotic translation initiation factor 4 gamma 1 isoform 4 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
eukaryotic translation initiation factor 4 gamma 1 isoform 6 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
matrin-3 isoform a [Homo sapiens]	0.77	2.01	17.85	4.09	4.67
matrin-3 isoform b [Homo sapiens]	0.77	2.01	17.85	4.09	4.67
cysteine--tRNA ligase, cytoplasmic isoform e [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform A [Homo sapiens]	0.26	1.96	0.88	1.37	0.76
elongation factor 1-delta isoform 1 [Homo sapiens]	0.25	0.83	0.71	0.44	0.67
elongation factor 1-delta isoform 5 [Homo sapiens]	1.82	0.83	1.34	1.64	2.16
glutathione reductase, mitochondrial isoform 2 precursor [Homo sapiens]	1.79	2.71	1.29	1.21	1.27
glutathione reductase, mitochondrial isoform 3 precursor [Homo sapiens]	1.79	2.45	1.30	1.20	1.29
glutathione reductase, mitochondrial isoform 4 precursor [Homo sapiens]	1.79	2.71	1.43	1.26	1.30
U6 snRNA phosphodiesterase isoform 2 [Homo sapiens]	4.07	0.73	0.50	0.33	0.50
serine/arginine-rich splicing factor 2 [Homo sapiens]	0.39	1.44	1.41	2.44	2.60
serine/arginine-rich splicing factor 7 isoform 2 [Homo sapiens]	1.68	0.67	0.45	0.43	0.66
interferon-induced 35 kDa protein [Homo sapiens]	0.64	0.97	2.76	1.35	1.48
spectrin alpha chain, non-erythrocytic 1 isoform 3 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
clathrin interactor 1 isoform 1 [Homo sapiens]	0.39	0.97	1.93	1.48	1.30
clathrin interactor 1 isoform 3 [Homo sapiens]	0.39	0.97	1.93	1.48	1.30
oxysterol-binding protein-related protein 9 isoform b [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
oxysterol-binding protein-related protein 9 isoform d [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
oxysterol-binding protein-related protein 9 isoform e [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
oxysterol-binding protein-related protein 9 isoform f [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
trypsin-3 isoform 4 preproprotein [Homo sapiens]	1.82	0.51	0.30	0.15	0.32
protein phosphatase 1 regulatory subunit 12B isoform g [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
dihydropyrimidinase-related protein 2 isoform 1 [Homo sapiens]	1.51	0.76	0.98	0.46	0.66
pyrin isoform 2 [Homo sapiens]	0.57	0.94	1.54	2.57	1.88
hydrocephalus-inducing protein homolog isoform c [Homo sapiens]	0.39	2.08	0.38	0.19	0.54

hydrocephalus-inducing protein homolog isoform d [Homo sapiens]	0.39	2.08	0.38	0.19	0.54
lamin-B1 isoform 2 [Homo sapiens]	0.26	0.99	0.95	2.15	0.68
nucleoside diphosphate kinase B isoform b [Homo sapiens]	3.26	1.51	1.69	1.94	1.62
histone-binding protein RBBP7 isoform 1 [Homo sapiens]	2.00	1.19	1.74	0.83	0.97
T-complex protein 1 subunit beta isoform 2 [Homo sapiens]	2.38	0.98	0.80	0.87	0.90
cullin-2 isoform a [Homo sapiens]	2.34	0.79	0.95	0.99	0.94
cullin-2 isoform b [Homo sapiens]	2.34	0.79	0.95	0.99	0.94
actin-related protein 2/3 complex subunit 4 isoform c [Homo sapiens]	0.77	2.71	1.87	1.89	2.34
ARPC4-TTL3 fusion protein [Homo sapiens]	0.75	1.40	0.76	0.57	0.94
copine-1 isoform c [Homo sapiens]	1.68	1.25	1.72	1.20	1.94
NAD kinase isoform 2 [Homo sapiens]	2.27	0.97	2.29	1.22	2.16
NAD kinase isoform 3 [Homo sapiens]	2.27	0.97	2.29	1.22	2.16
malate dehydrogenase, cytoplasmic isoform 1 [Homo sapiens]	3.47	1.22	1.62	0.55	1.31
malate dehydrogenase, cytoplasmic isoform 3 [Homo sapiens]	3.43	1.22	1.62	0.55	1.31
NLR family CARD domain-containing protein 4 [Homo sapiens]	0.98	0.83	0.76	1.26	0.77
lactotransferrin isoform 2 [Homo sapiens]	0.77	5.05	0.84	1.31	2.38
26S protease regulatory subunit 8 isoform 2 [Homo sapiens]	7.36	0.85	0.62	0.62	0.58
adenylate kinase 2, mitochondrial isoform c [Homo sapiens]	1.18	1.26	1.69	1.69	1.27
leukotriene-B(4) omega-hydroxylase 2 isoform b [Homo sapiens]	0.69	2.32	0.88	0.51	1.37
stathmin-2 isoform 1 [Homo sapiens]	1.34	0.93	1.51	2.22	1.29
PMF1-BGLAP protein isoform 4 [Homo sapiens]	0.23	0.84	0.42	0.23	0.62
mitochondrial peptide methionine sulfoxide reductase isoform d [Homo sapiens]	0.83	1.90	2.29	1.27	0.94
cathepsin S isoform 2 preproprotein [Homo sapiens]	0.41	1.34	1.87	0.71	1.45
SAA2-SAA2 protein precursor [Homo sapiens]	0.18	0.93	0.57	0.33	0.58
serum amyloid A-4 protein precursor [Homo sapiens]	0.18	0.93	0.57	0.33	0.58
proteasome subunit alpha type-5 isoform 2 [Homo sapiens]	1.71	1.44	0.62	0.44	0.62
proteasome subunit beta type-2 isoform 3 [Homo sapiens]	3.34	0.81	1.48	0.49	0.63
proteasome subunit beta type-2 isoform 2 [Homo sapiens]	3.34	2.08	1.48	0.49	0.63
60S ribosomal protein L11 isoform 2 [Homo sapiens]	1.47	1.47	1.38	1.73	1.54
NEDD8-MDP1 protein [Homo sapiens]	1.82	1.62	1.39	2.38	1.27
gamma-glutamylcyclotransferase isoform 2 [Homo sapiens]	1.18	1.34	1.38	0.81	1.78
gamma-glutamylcyclotransferase isoform 3 [Homo sapiens]	1.18	1.34	1.38	0.81	1.78
gamma-glutamylcyclotransferase isoform 4 [Homo sapiens]	4.99	1.34	1.41	1.34	1.78
voltage-gated potassium channel subunit beta-2 isoform 3 [Homo sapiens]	0.88	1.98	1.91	2.37	1.86
voltage-gated potassium channel subunit beta-2 isoform 4 [Homo sapiens]	0.88	1.98	1.91	2.37	1.86
huntingtin-interacting protein K isoform 2 [Homo sapiens]	0.25	0.66	2.29	1.00	0.78
actin, gamma-enteric smooth muscle isoform 2 precursor [Homo sapiens]	2.79	0.94	0.49	0.31	0.69
actin, cytoplasmic 2 [Homo sapiens]	0.80	1.44	1.26	1.23	1.19
wiskott-Aldrich syndrome protein family member 2	2.79	0.84	0.85	0.51	0.93

isoform 2 [Homo sapiens]

coronin-7 isoform 2 [Homo sapiens]	0.39	0.77	0.64	0.70	0.84
coronin-7 isoform 3 [Homo sapiens]	0.39	0.77	0.64	0.70	0.84
CORO7-PAM16 protein [Homo sapiens]	0.39	0.77	0.64	0.70	0.84
c-myc promoter-binding protein-1 isoform MBP-1 [Homo sapiens]	0.88	1.24	1.29	1.19	1.21
complement factor H-related protein 4 isoform 1 precursor [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
complement factor H-related protein 4 isoform 2 precursor [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
alcohol dehydrogenase [NADP(+)] [Homo sapiens]	1.64	0.97	1.18	1.24	1.38
adenosine kinase isoform c [Homo sapiens]	6.44	1.96	2.00	2.55	1.33
adenosine kinase isoform d [Homo sapiens]	3.56	1.90	1.21	1.30	1.28
RPS10-NUDT3 protein [Homo sapiens]	0.91	1.21	1.93	2.72	1.99
HSPE1-MOB4 protein [Homo sapiens]	0.66	1.00	2.31	1.43	1.25
scaffold attachment factor B1 isoform 1 [Homo sapiens]	0.52	1.25	3.48	7.80	1.40
scaffold attachment factor B1 isoform 2 [Homo sapiens]	0.52	1.25	3.48	7.80	1.40
scaffold attachment factor B1 isoform 4 [Homo sapiens]	0.52	1.25	3.48	7.80	1.40
CD44 antigen isoform 6 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 7 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
CD44 antigen isoform 8 precursor [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
extracellular matrix protein 1 isoform 3 precursor [Homo sapiens]	1.18	0.99	0.44	0.23	0.62
40S ribosomal protein S10 [Homo sapiens]	0.91	1.21	1.93	2.72	1.99
vitamin D-binding protein isoform 1 precursor [Homo sapiens]	0.31	0.93	0.48	0.27	0.57
vitamin D-binding protein isoform 3 precursor [Homo sapiens]	0.31	0.93	0.48	0.27	0.57
ribose-phosphate pyrophosphokinase 1 isoform 2 [Homo sapiens]	5.15	1.44	0.70	0.69	0.84
arachidonate 5-lipoxygenase-activating protein isoform 2 [Homo sapiens]	7.95	0.93	0.55	0.41	0.62
calcium/calmodulin-dependent protein kinase type II subunit gamma isoform 7 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
eukaryotic initiation factor 4A-I isoform 2 [Homo sapiens]	2.00	2.08	1.95	2.80	1.42
transcription elongation factor B polypeptide 1 isoform a [Homo sapiens]	2.17	1.00	1.72	1.35	0.96
transcription elongation factor B polypeptide 1 isoform b [Homo sapiens]	2.17	1.00	1.72	1.35	0.96
syntaxin-16 isoform e [Homo sapiens]	4.35	2.32	0.51	0.30	0.45
aldehyde dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
nesprin-1 isoform 1 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
F-actin-capping protein subunit beta isoform 2 [Homo sapiens]	0.66	1.40	1.34	1.70	1.94
F-actin-capping protein subunit beta isoform 3 [Homo sapiens]	0.62	1.30	1.21	1.54	1.74
gamma-interferon-inducible protein 16 isoform 1 [Homo sapiens]	0.35	0.64	0.33	0.30	0.44
5'-AMP-activated protein kinase subunit gamma-1 isoform 3 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
5'-AMP-activated protein kinase subunit gamma-1 isoform 4 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
NSFL1 cofactor p47 isoform d [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
pyruvate kinase PKM isoform c [Homo sapiens]	0.83	0.94	1.62	1.72	1.27
pyruvate kinase PKM isoform d [Homo sapiens]	0.88	0.95	1.54	1.54	1.26

pyruvate kinase PKM isoform e [Homo sapiens]	0.88	0.93	1.55	1.59	1.23
pyruvate kinase PKM isoform f [Homo sapiens]	0.83	0.94	1.62	1.72	1.27
ras-related protein Rab-11A isoform 2 [Homo sapiens]	1.64	1.94	1.31	1.35	1.53
trans-Golgi network integral membrane protein 2 isoform 2 precursor [Homo sapiens]	0.25	0.95	0.71	0.52	0.76
trans-Golgi network integral membrane protein 2 isoform 3 precursor [Homo sapiens]	0.25	0.95	0.71	0.52	0.76
trans-Golgi network integral membrane protein 2 isoform 4 precursor [Homo sapiens]	0.25	0.95	0.71	0.52	0.76
retinal dehydrogenase 2 isoform 4 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
phosphatidylinositol-binding clathrin assembly protein isoform 3 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
protein phosphatase 2, regulatory subunit B, gamma isoform c [Homo sapiens]	1.64	0.89	0.85	0.80	0.80
protein phosphatase 2, regulatory subunit B, gamma isoform d [Homo sapiens]	1.64	0.89	0.85	0.80	0.80
nascent polypeptide-associated complex subunit alpha isoform a [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
attractin isoform 4 [Homo sapiens]	0.35	0.93	0.35	0.21	0.55
basic leucine zipper and W2 domain-containing protein 1 isoform 1 [Homo sapiens]	2.17	1.30	1.64	4.43	2.27
basic leucine zipper and W2 domain-containing protein 1 isoform 2 [Homo sapiens]	2.17	1.30	1.64	4.43	2.27
basic leucine zipper and W2 domain-containing protein 1 isoform 3 [Homo sapiens]	2.17	1.30	1.64	4.43	2.27
vascular non-inflammatory molecule 2 isoform 3 precursor [Homo sapiens]	0.50	0.80	0.43	0.29	0.78
glial fibrillary acidic protein isoform 3 [Homo sapiens]	0.57	0.81	0.83	1.44	0.51
twinfilin-1 isoform 2 [Homo sapiens]	2.00	1.19	1.70	2.75	1.41
twinfilin-1 isoform 1 [Homo sapiens]	2.00	1.19	1.70	2.75	1.41
ras-related protein Rab-2A isoform b [Homo sapiens]	0.52	1.90	3.91	3.36	1.96
cAMP-dependent protein kinase catalytic subunit beta isoform 4 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
cAMP-dependent protein kinase catalytic subunit beta isoform 5 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
cAMP-dependent protein kinase catalytic subunit beta isoform 6 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
cAMP-dependent protein kinase catalytic subunit beta isoform 7 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
cAMP-dependent protein kinase catalytic subunit beta isoform 8 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
cAMP-dependent protein kinase catalytic subunit beta isoform 9 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
complement C4-B-like preproprotein [Homo sapiens]	0.69	0.97	0.57	0.32	0.74
phospholipid transfer protein isoform c precursor [Homo sapiens]	1.61	1.97	0.66	0.46	0.80
phospholipid transfer protein isoform d [Homo sapiens]	1.21	2.37	0.71	0.57	0.80
lymphocyte-specific protein 1 isoform 3 [Homo sapiens]	0.28	0.81	0.64	0.91	0.88
sorting nexin-1 isoform d [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
septin-7 isoform 3 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
HLA class I histocompatibility antigen, Cw-1 alpha chain precursor [Homo sapiens]	0.83	0.96	0.67	0.34	0.80
apolipoprotein B receptor [Homo sapiens]	0.64	0.83	0.97	2.25	1.54
FYN-binding protein isoform 3 [Homo sapiens]	1.71	1.63	0.81	0.79	0.94
fructose-bisphosphate aldolase A isoform 2 [Homo sapiens]	1.51	1.73	2.49	0.98	1.61
trypsin-3 isoform 3 preproprotein [Homo sapiens]	1.82	0.51	0.30	0.15	0.32
EF-hand domain-containing protein D1 isoform 2 [Homo sapiens]	0.62	0.85	0.94	0.64	0.89

cofilin-2 isoform 2 [Homo sapiens]	0.91	1.26	1.55	1.72	1.38
ras-related protein Rab-6A isoform c [Homo sapiens]	2.76	2.10	4.73	6.76	3.09
regulator complex protein LAMTOR3 isoform 2 [Homo sapiens]	5.93	3.82	6.46	6.72	3.39
scavenger receptor cysteine-rich type 1 protein M130 isoform a precursor [Homo sapiens]	2.34	1.53	1.29	2.17	1.63
scavenger receptor cysteine-rich type 1 protein M130 isoform b precursor [Homo sapiens]	2.34	1.53	1.29	2.17	1.63
apoptosis inhibitor 5 isoform d [Homo sapiens]	0.75	1.18	1.29	1.40	1.74
tumor protein D54 isoform g [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform h [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
tumor protein D54 isoform j [Homo sapiens]	0.39	2.71	0.88	0.80	2.34
MAP kinase-activated protein kinase 3 [Homo sapiens]	0.64	1.96	1.18	1.58	1.19
phosphoribosyl pyrophosphate synthase-associated protein 2 isoform 4 [Homo sapiens]	6.63	1.41	1.45	1.37	0.96
phosphoribosyl pyrophosphate synthase-associated protein 2 isoform 2 [Homo sapiens]	6.63	1.41	1.45	1.37	0.96
E3 ubiquitin-protein ligase NEDD4-like isoform 7 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
DNA-(apurinic or apyrimidinic site) lyase [Homo sapiens]	0.95	1.44	1.58	2.10	1.56
arginase-1 isoform 1 [Homo sapiens]	2.79	1.00	0.92	1.77	1.45
BH3-interacting domain death agonist isoform 3 [Homo sapiens]	1.57	0.74	0.97	0.98	1.00
C7orf55-LUC7L2 protein [Homo sapiens]	0.45	0.77	0.63	0.52	0.58
putative RNA-binding protein Luc7-like 2 isoform 3 [Homo sapiens]	0.45	0.77	0.63	0.52	0.58
dihydropyrimidinase-related protein 2 isoform 3 [Homo sapiens]	1.51	0.76	0.98	0.46	0.66
UV excision repair protein RAD23 homolog B isoform 2 [Homo sapiens]	2.27	0.96	1.62	2.17	2.01
UV excision repair protein RAD23 homolog B isoform 3 [Homo sapiens]	1.47	0.96	1.24	1.51	0.99
low affinity immunoglobulin gamma Fc region receptor III-B isoform 1 [Homo sapiens]	0.54	2.08	2.56	1.18	4.26
cathelicidin antimicrobial peptide preproprotein [Homo sapiens]	0.23	2.72	2.07	1.28	2.51
MOB kinase activator 1B isoform 3 [Homo sapiens]	1.71	0.96	1.29	1.44	0.94
polypyrimidine tract-binding protein 3 isoform 4 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
polypyrimidine tract-binding protein 3 isoform 5 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
polypyrimidine tract-binding protein 3 isoform 6 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
thioredoxin isoform 2 [Homo sapiens]	3.52	0.98	1.19	1.68	1.48
serine/threonine-protein phosphatase PP1-gamma catalytic subunit isoform 2 [Homo sapiens]	0.41	0.91	0.48	0.34	0.52
protein phosphatase 1 regulatory subunit 12A isoform c [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
protein phosphatase 1 regulatory subunit 12A isoform d [Homo sapiens]	0.43	0.91	0.91	1.38	1.81
protein SET isoform 3 [Homo sapiens]	0.88	0.97	1.68	1.98	0.96
protein SET isoform 4 [Homo sapiens]	0.88	0.97	1.68	1.98	0.96
ras-related protein Rap-1b isoform 2 [Homo sapiens]	1.64	1.40	1.91	1.93	1.42
ras-related protein Rap-1b isoform 3 [Homo sapiens]	0.98	1.39	1.87	2.08	1.45
ras-related protein Rap-1b isoform 4 [Homo sapiens]	0.88	1.40	1.91	2.24	1.50
ras-related protein Rab-5B isoform 2 [Homo sapiens]	0.77	1.58	2.79	4.19	1.35
ras-related protein Rab-5C isoform b [Homo sapiens]	0.77	2.27	4.15	6.77	1.52
protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 2 [Homo sapiens]	4.35	2.08	1.24	1.36	2.39

protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 3 [Homo sapiens]	4.40	1.73	1.18	1.24	1.61
protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 4 [Homo sapiens]	3.75	2.20	1.21	1.18	1.29
protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 5 [Homo sapiens]	4.40	1.73	1.18	1.24	1.61
ubiquitin carboxyl-terminal hydrolase 15 isoform 1 [Homo sapiens]	6.25	1.00	0.95	1.40	0.82
ubiquitin carboxyl-terminal hydrolase 15 isoform 3 [Homo sapiens]	8.60	1.25	1.51	2.51	1.20
clusterin preproprotein [Homo sapiens]	0.26	0.52	0.30	0.14	0.40
complement C4-A isoform 2 preproprotein [Homo sapiens]	0.35	0.93	0.52	0.30	0.77
heterogeneous nuclear ribonucleoprotein Q isoform 7 [Homo sapiens]	3.86	0.70	1.54	1.29	0.81
biliverdin reductase A precursor [Homo sapiens]	7.30	0.96	1.21	1.25	0.85
GDP-mannose 4,6 dehydratase isoform 2 [Homo sapiens]	2.19	0.96	2.09	2.06	1.39
myosin-10 isoform 2 [Homo sapiens]	0.95	0.94	1.43	1.74	2.45
myosin-10 isoform 3 [Homo sapiens]	0.95	0.94	1.43	1.74	2.45
N-alpha-acetyltransferase 10 isoform 2 [Homo sapiens]	0.52	1.73	6.21	9.21	2.53
N-alpha-acetyltransferase 10 isoform 3 [Homo sapiens]	0.52	1.73	6.21	9.21	2.53
exportin-2 isoform 2 [Homo sapiens]	1.18	0.89	0.97	1.56	2.39
macrophage-capping protein isoform 2 [Homo sapiens]	0.45	1.73	1.44	1.64	1.44
apolipoprotein M isoform 2 [Homo sapiens]	0.26	0.57	0.30	0.18	0.45
sorting nexin-12 isoform 3 [Homo sapiens]	3.90	0.91	0.99	1.35	0.96
programmed cell death 6-interacting protein isoform 3 [Homo sapiens]	1.96	0.74	0.98	0.96	0.81
arachidonate 5-lipoxygenase isoform 2 [Homo sapiens]	2.79	2.08	1.24	2.39	1.30
arachidonate 5-lipoxygenase isoform 3 [Homo sapiens]	2.79	0.83	0.88	1.18	0.90
protein flightless-1 homolog isoform 2 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
protein flightless-1 homolog isoform 3 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
keratin, type II cytoskeletal 8 isoform 1 [Homo sapiens]	0.62	0.25	0.34	0.27	0.18
keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]	0.62	0.25	0.34	0.27	0.18
immunoglobulin lambda-like polypeptide 5 isoform 2 [Homo sapiens]	0.31	0.77	0.34	0.18	0.70
ubiquitin-conjugating enzyme E2 L3 isoform 3 [Homo sapiens]	2.38	0.94	1.27	1.56	1.82
ubiquitin-conjugating enzyme E2 L3 isoform 4 [Homo sapiens]	2.38	0.94	1.27	1.56	1.82
SAM domain-containing protein SAMSN-1 isoform 2 [Homo sapiens]	0.19	1.47	0.79	0.85	0.83
ras-related protein Rab-18 isoform 2 [Homo sapiens]	0.56	0.85	0.83	0.95	0.64
ras-related protein Rab-18 isoform 3 [Homo sapiens]	0.69	0.92	0.83	2.21	0.74
ras-related protein Rab-18 isoform 5 [Homo sapiens]	0.56	0.85	0.83	0.95	0.64
guanine nucleotide-binding protein G(i) subunit alpha-1 isoform 2 [Homo sapiens]	2.00	1.19	2.02	2.08	1.34
single-stranded DNA-binding protein, mitochondrial precursor [Homo sapiens]	0.66	1.51	0.71	0.53	0.78
leukotriene A-4 hydrolase isoform 3 [Homo sapiens]	0.91	1.19	1.26	0.89	1.42
leukotriene A-4 hydrolase isoform 2 [Homo sapiens]	0.88	2.08	1.29	0.92	1.88
dipeptidyl peptidase 3 isoform 2 [Homo sapiens]	1.37	0.91	0.58	0.43	0.70
T-complex protein 1 subunit delta isoform b [Homo sapiens]	5.56	1.18	1.39	1.60	1.20
casein kinase 2, alpha 1 polypeptide-like [Homo sapiens]	20.10	1.24	0.75	0.84	1.83

U4/U6.U5 tri-snRNP-associated protein 2 isoform 2 [Homo sapiens]	0.41	1.34	1.42	1.80	1.25
U4/U6.U5 tri-snRNP-associated protein 2 isoform 3 [Homo sapiens]	0.41	1.34	1.42	1.80	1.25
U4/U6.U5 tri-snRNP-associated protein 2 isoform 4 [Homo sapiens]	0.41	1.34	1.42	1.80	1.25
glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]	2.00	1.24	1.78	0.98	1.58
40S ribosomal protein S3 isoform 1 [Homo sapiens]	1.96	0.99	0.95	1.23	2.39
sorcin isoform C [Homo sapiens]	14.12	0.75	0.66	0.69	1.61
sorcin isoform D [Homo sapiens]	14.12	0.75	0.66	0.69	1.61
probable ATP-dependent RNA helicase DDX6 [Homo sapiens]	0.83	1.47	1.58	2.00	1.33
cullin-3 isoform 3 [Homo sapiens]	1.00	0.94	0.62	0.66	0.51
vesicle-trafficking protein SEC22b precursor [Homo sapiens]	0.95	1.82	2.74	5.16	1.75
heterogeneous nuclear ribonucleoprotein H [Homo sapiens]	4.84	1.69	2.26	3.89	1.47
beta-arrestin-2 isoform 4 [Homo sapiens]	1.00	1.17	1.53	2.55	1.61
beta-arrestin-2 isoform 3 [Homo sapiens]	1.31	1.25	1.44	2.25	1.45
beta-arrestin-2 isoform 5 [Homo sapiens]	1.31	1.25	1.44	2.25	1.45
beta-arrestin-2 isoform 6 [Homo sapiens]	1.31	1.25	1.44	2.25	1.45
ATP synthase subunit alpha, mitochondrial isoform b precursor [Homo sapiens]	2.46	0.88	1.37	0.64	0.68
AMP deaminase 2 isoform 1 [Homo sapiens]	1.34	0.88	0.66	0.75	0.91
AMP deaminase 2 isoform 4 [Homo sapiens]	1.34	0.88	0.66	0.75	0.91
lamin isoform D [Homo sapiens]	0.31	0.08	0.14	0.05	0.13
ubiquitin-conjugating enzyme E2 variant 1 isoform c [Homo sapiens]	13.07	1.31	2.09	1.94	1.68
ubiquitin-conjugating enzyme E2 variant 1 isoform e [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
ubiquitin-conjugating enzyme E2 variant 1 isoform f [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
protein crumbs homolog 1 isoform 3 [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
protein crumbs homolog 1 isoform 4 precursor [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
thymidine phosphorylase isoform 2 proprotein [Homo sapiens]	1.41	0.99	1.54	0.85	2.01
ankyrin repeat and FYVE domain-containing protein 1 isoform 3 [Homo sapiens]	1.31	1.51	1.72	1.21	1.28
COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]	4.38	1.22	2.47	1.69	2.30
triosephosphate isomerase isoform 3 [Homo sapiens]	2.02	1.27	1.34	1.35	1.45
transketolase isoform 2 [Homo sapiens]	0.69	1.26	1.80	1.55	1.46
histidine--tRNA ligase, cytoplasmic isoform 2 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
histidine--tRNA ligase, cytoplasmic isoform 3 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
histidine--tRNA ligase, cytoplasmic isoform 4 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
proto-oncogene vav isoform 2 [Homo sapiens]	1.68	0.91	0.65	0.73	0.80
proto-oncogene vav isoform 3 [Homo sapiens]	0.75	0.88	0.56	0.52	0.78
porphobilinogen deaminase isoform 3 [Homo sapiens]	11.91	0.64	0.55	0.24	0.64
porphobilinogen deaminase isoform 4 [Homo sapiens]	11.91	0.64	0.55	0.24	0.64
selenium-binding protein 1 isoform 2 [Homo sapiens]	42.28	0.81	0.66	0.30	0.78
selenium-binding protein 1 isoform 3 [Homo sapiens]	2.31	0.82	0.67	0.35	0.81
minor histocompatibility protein HA-1 isoform 2 precursor [Homo sapiens]	0.45	0.68	0.50	0.79	0.75
116 kDa U5 small nuclear ribonucleoprotein component isoform a [Homo sapiens]	1.31	0.73	0.65	0.67	0.70

116 kDa U5 small nuclear ribonucleoprotein component isoform c [Homo sapiens]	1.31	0.73	0.65	0.67	0.70
UPF0687 protein C20orf27 isoform 2 [Homo sapiens]	4.19	1.37	2.56	1.81	1.25
polycystic kidney disease 2-like 2 protein isoform 2 [Homo sapiens]	0.19	0.61	0.39	0.20	0.67
polycystic kidney disease 2-like 2 protein isoform 3 [Homo sapiens]	0.19	0.61	0.39	0.20	0.67
threonine--tRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	1.24	0.76	1.54	0.98	1.00
threonine--tRNA ligase, cytoplasmic isoform 2 [Homo sapiens]	1.24	0.76	1.54	0.98	1.00
spermine synthase isoform 2 [Homo sapiens]	2.00	0.98	0.75	0.63	0.85
radixin isoform 1 [Homo sapiens]	3.30	0.91	0.61	0.35	0.66
radixin isoform 5 [Homo sapiens]	3.30	0.91	0.61	0.35	0.66
signal recognition particle subunit SRP68 isoform 2 [Homo sapiens]	0.14	1.80	4.51	9.45	3.31
translin isoform 2 [Homo sapiens]	1.61	1.25	1.91	1.70	1.44
40S ribosomal protein S3 isoform 2 [Homo sapiens]	1.96	0.99	0.95	1.23	2.39
40S ribosomal protein S3 isoform 3 [Homo sapiens]	4.60	0.91	0.88	0.94	2.39
dynactin subunit 2 isoform 2 [Homo sapiens]	2.66	0.94	0.94	0.85	0.87
dynactin subunit 2 isoform 3 [Homo sapiens]	2.66	0.94	0.94	0.85	0.87
thioredoxin reductase 1, cytoplasmic isoform 4 [Homo sapiens]	1.76	1.41	1.68	1.87	1.75
thioredoxin reductase 1, cytoplasmic isoform 5 [Homo sapiens]	1.76	1.41	1.68	1.87	1.75
AP-3 complex subunit delta-1 isoform 3 [Homo sapiens]	0.98	2.09	2.18	3.20	1.73
reticulon-3 isoform e [Homo sapiens]	0.67	0.80	0.54	0.57	0.62
reticulon-3 isoform f [Homo sapiens]	0.67	0.80	0.54	0.57	0.62
lamin-B2 [Homo sapiens]	0.16	0.67	0.67	1.36	0.52
chitotriosidase-1 isoform 2 precursor [Homo sapiens]	0.77	1.62	0.97	0.82	1.59
ras-related protein Rab-44 [Homo sapiens]	0.11	0.97	1.30	2.31	1.61
signal recognition particle subunit SRP72 isoform 2 [Homo sapiens]	0.45	0.78	0.56	0.64	0.65
receptor-type tyrosine-protein phosphatase C isoform 1 precursor [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
receptor-type tyrosine-protein phosphatase C isoform 2 precursor [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
eukaryotic translation initiation factor 6 isoform a [Homo sapiens]	6.25	0.91	0.64	0.39	0.82
interleukin enhancer-binding factor 2 isoform 2 [Homo sapiens]	0.75	0.91	1.68	1.69	0.83
UV excision repair protein RAD23 homolog A isoform 2 [Homo sapiens]	1.34	0.78	0.40	0.21	0.57
UV excision repair protein RAD23 homolog A isoform 3 [Homo sapiens]	1.34	0.78	0.40	0.21	0.57
tubulin alpha-1A chain isoform 1 [Homo sapiens]	1.00	0.73	0.99	0.51	0.84
tubulin alpha-1A chain isoform 2 [Homo sapiens]	1.00	0.73	0.99	0.51	0.84
actin-related protein 2/3 complex subunit 5 isoform 2 [Homo sapiens]	0.75	1.40	1.46	1.82	1.21
very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 3 [Homo sapiens]	0.31	0.65	0.75	0.39	0.62
very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 4 [Homo sapiens]	0.31	0.65	0.75	0.39	0.62
proteasome subunit beta type-6 isoform 2 proprotein [Homo sapiens]	2.79	1.40	0.63	0.49	0.81
26S proteasome non-ATPase regulatory subunit 11 [Homo sapiens]	1.24	0.87	0.71	0.77	0.83
chitotriosidase-1 isoform 3 precursor [Homo sapiens]	0.45	1.38	0.75	0.77	1.40
putative RNA-binding protein Luc7-like 2 isoform 4 [Homo sapiens]	0.45	0.77	0.63	0.52	0.58

bcl-2-like protein 13 isoform b [Homo sapiens]	0.83	0.81	0.50	0.46	0.62
bcl-2-like protein 13 isoform c [Homo sapiens]	0.83	0.81	0.50	0.46	0.62
bcl-2-like protein 13 isoform h [Homo sapiens]	0.83	0.81	0.50	0.46	0.62
hydrocephalus-inducing protein homolog isoform a [Homo sapiens]	0.39	2.08	0.38	0.19	0.54
ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 1 [Homo sapiens]	1.64	0.69	0.46	0.44	0.67
low affinity immunoglobulin gamma Fc region receptor III-B isoform 3 [Homo sapiens]	0.54	2.08	2.56	1.18	4.26
low affinity immunoglobulin gamma Fc region receptor III-B isoform 4 [Homo sapiens]	0.54	2.08	2.56	1.18	4.26
low affinity immunoglobulin gamma Fc region receptor III-B isoform 5 [Homo sapiens]	0.50	1.58	0.81	0.78	2.78
brain acid soluble protein 1 [Homo sapiens]	0.23	0.94	1.61	1.92	0.79
PREDICTED: low affinity immunoglobulin gamma Fc region receptor III-A-like isoform X1 [Homo sapiens]	0.54	2.31	1.74	2.45	7.01
PREDICTED: nuclear transport factor 2-like [Homo sapiens]	29.69	1.26	2.28	2.52	2.02
PREDICTED: prothymosin alpha-like [Homo sapiens]	0.88	1.96	2.01	1.97	0.43
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	1.31	1.90	2.68	2.33	1.63
LIM and SH3 domain protein 1 isoform b [Homo sapiens]	1.61	0.64	0.45	0.24	0.50
zinc finger CCCH-type domain-containing-like [Homo sapiens]		0.43	0.51	1.37	0.50
putative macrophage stimulating 1-like protein [Homo sapiens]	0.56	0.84	0.61	0.32	0.70
26S proteasome non-ATPase regulatory subunit 6 isoform 1 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
26S proteasome non-ATPase regulatory subunit 6 isoform 3 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
26S proteasome non-ATPase regulatory subunit 6 isoform 4 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
cytoplasmic dynein 1 intermediate chain 2 isoform 2 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
cytoplasmic dynein 1 intermediate chain 2 isoform 1 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
cytoplasmic dynein 1 intermediate chain 2 isoform 3 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
serpin B6 isoform c [Homo sapiens]	1.54	2.71	1.19	0.96	2.68
serpin B6 isoform d [Homo sapiens]	1.54	2.71	1.19	0.96	2.68
serpin B6 isoform a [Homo sapiens]	1.54	2.71	1.19	0.96	2.68
serine/threonine-protein phosphatase 2A activator isoform f [Homo sapiens]	9.83	1.00	1.18	1.25	0.89
KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 2 [Homo sapiens]	2.79	0.76	1.96	1.36	0.97
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform e [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform d [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform a [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform g [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform isoform f [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
heat shock protein HSP 90-beta isoform b [Homo sapiens]	2.00	1.62	0.99	0.94	1.35

heat shock protein HSP 90-beta isoform c [Homo sapiens]	1.21	1.62	1.43	1.33	0.93
serine/threonine-protein kinase 25 isoform 1 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
serine/threonine-protein kinase 25 isoform 2 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
syntaxin-binding protein 2 isoform c [Homo sapiens]	1.44	0.98	1.58	2.21	1.28
ras-related protein Rab-13 isoform 2 [Homo sapiens]	1.61	1.51	1.21	1.20	1.42
glutamine--tRNA ligase isoform b [Homo sapiens]	10.98	1.34	0.69	0.45	0.95
cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b [Homo sapiens]	0.64	1.62	0.82	0.79	0.89
importin subunit beta-1 isoform 2 [Homo sapiens]	1.37	0.89	2.07	1.28	1.61
serpin B8 isoform c [Homo sapiens]	1.00	1.30	1.18	1.33	1.82
POTE ankyrin domain family member J [Homo sapiens]	0.62	1.30	1.18	1.26	1.94
actin-related protein 3 isoform 2 [Homo sapiens]	1.31	2.45	1.38	1.27	1.61
transgelin-2 isoform b [Homo sapiens]	2.33	0.88	1.00	0.94	1.94
transgelin-2 isoform a [Homo sapiens]	2.33	0.88	1.00	0.94	1.94
POTE ankyrin domain family member I [Homo sapiens]	0.66	0.91	0.53	0.37	0.79
stromal interaction molecule 1 isoform 1 precursor [Homo sapiens]	0.33	0.93	0.65	1.33	0.76
stromal interaction molecule 1 isoform 3 precursor [Homo sapiens]	0.46	0.96	0.52	0.51	0.67
tropomyosin alpha-3 chain isoform 6 [Homo sapiens]	0.52	1.19	2.49	1.76	1.30
tropomyosin alpha-3 chain isoform 7 [Homo sapiens]	0.91	1.90	0.88	2.17	0.92
tropomyosin alpha-3 chain isoform 8 [Homo sapiens]	0.91	1.90	0.88	2.17	0.92
tropomyosin alpha-3 chain isoform 9 [Homo sapiens]	1.34	1.21	1.91	5.18	1.71
neutral alpha-glucosidase AB isoform 4 [Homo sapiens]	1.41	1.44	2.21	1.62	1.23
neutral alpha-glucosidase AB isoform 5 [Homo sapiens]	2.38	1.51	2.25	1.72	1.40
neutral alpha-glucosidase AB isoform 6 [Homo sapiens]	2.38	1.51	2.25	1.72	1.40
sorting nexin-2 isoform 2 [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
dynammin-3 isoform c [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
ribulose-phosphate 3-epimerase isoform 3 [Homo sapiens]	0.39	0.62	0.61	0.62	0.74
alpha-actinin-2 isoform 2 [Homo sapiens]	0.91	0.96	2.35	1.74	0.90
alpha-actinin-2 isoform 3 [Homo sapiens]	0.91	0.96	2.35	1.74	0.90
annexin A11 isoform 2 [Homo sapiens]	0.88	1.24	2.16	0.96	1.44
integrin-linked protein kinase isoform 2 [Homo sapiens]	0.28	0.63	0.51	0.57	0.54
cullin-4A isoform 2 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
cullin-4A isoform 3 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
AP-3 complex subunit beta-2 isoform 3 [Homo sapiens]	0.77	2.30	1.42	0.45	2.60
AP-3 complex subunit beta-2 isoform 1 [Homo sapiens]	0.77	2.30	1.42	0.45	2.60
carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	0.69	0.58	0.41	0.19	0.46
carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	0.77	0.62	0.42	0.22	0.46
mitogen-activated protein kinase 8 JNK1 beta2 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
mitogen-activated protein kinase 8 isoform 5 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
actin-related protein 2/3 complex subunit 3 isoform 1 [Homo sapiens]	0.95	1.21	2.49	2.74	1.30
complement component C8 beta chain isoform 1	0.33	2.08	0.52	0.31	0.53

preproprotein [Homo sapiens]					
complement component C8 beta chain isoform 2 [Homo sapiens]	0.33	2.08	0.52	0.31	0.53
complement component C8 beta chain isoform 3 [Homo sapiens]	0.33	2.08	0.52	0.31	0.53
ran-specific GTPase-activating protein isoform 1 [Homo sapiens]	15.50	0.70	2.26	1.24	0.78
ran-specific GTPase-activating protein isoform 3 [Homo sapiens]	15.50	0.70	2.26	1.24	0.78
ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	15.50	0.70	2.26	1.24	0.78
small nuclear ribonucleoprotein Sm D3 [Homo sapiens]	0.77	1.39	1.18	1.98	1.22
26S proteasome non-ATPase regulatory subunit 2 isoform 2 [Homo sapiens]	2.27	0.93	0.76	0.79	0.90
26S proteasome non-ATPase regulatory subunit 2 isoform 3 [Homo sapiens]	2.83	0.97	1.78	1.40	1.23
probable histidine--tRNA ligase, mitochondrial isoform 2 [Homo sapiens]	4.55	1.00	1.26	1.44	2.76
probable histidine--tRNA ligase, mitochondrial isoform 3 [Homo sapiens]	4.55	1.00	1.26	1.44	2.76
ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]	2.76	0.88	1.56	4.80	1.31
acyl-protein thioesterase 1 isoform 2 [Homo sapiens]	0.91	0.98	1.78	1.23	1.23
acyl-protein thioesterase 1 isoform 3 [Homo sapiens]	0.80	0.79	0.82	0.99	0.90
acyl-protein thioesterase 1 isoform 4 [Homo sapiens]	2.38	0.85	0.97	1.25	1.23
acyl-protein thioesterase 1 isoform 6 [Homo sapiens]	0.80	0.79	0.82	0.99	0.90
protein SEC13 homolog isoform 5 [Homo sapiens]	1.00	1.24	1.29	1.68	1.30
copine-6 isoform 1 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 4 [Homo sapiens]	0.95	0.80	0.83	1.97	0.90
acidic leucine-rich nuclear phosphoprotein 32 family member E isoform 5 [Homo sapiens]	0.57	0.77	0.50	0.95	0.64
endothelial differentiation-related factor 1 isoform 3 [Homo sapiens]	0.56	0.85	0.95	0.97	1.82
endothelial differentiation-related factor 1 isoform 4 [Homo sapiens]	0.56	0.85	0.95	0.97	1.82
endothelial differentiation-related factor 1 isoform 5 [Homo sapiens]	0.56	0.85	0.95	0.97	1.82
structural maintenance of chromosomes protein 1A isoform 2 [Homo sapiens]	0.45	0.96	0.97	1.37	1.28
beta-catenin-like protein 1 isoform 2 [Homo sapiens]	7.48	2.29	2.24	4.58	2.50
neutrophil cytosol factor 1 [Homo sapiens]	0.95	0.67	0.85	1.47	1.74
centrosomal protein of 85 kDa isoform 2 [Homo sapiens]	732.97	0.96	3.92	0.88	2.50
proteasome activator complex subunit 1 isoform 3 [Homo sapiens]	1.61	0.89	0.98	0.97	1.17
proteasome activator complex subunit 1 isoform 4 [Homo sapiens]	3.34	0.89	1.31	1.43	0.99
trifunctional enzyme subunit beta, mitochondrial isoform 2 precursor [Homo sapiens]	0.43	0.81	1.00	0.43	4.36
trifunctional enzyme subunit beta, mitochondrial isoform 3 [Homo sapiens]	0.43	0.81	1.00	0.43	4.36
polyubiquitin-B precursor [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
biotinidase isoform 1 [Homo sapiens]	0.06	0.49	0.17	0.13	0.24
biotinidase isoform 2 [Homo sapiens]	0.06	0.49	0.17	0.13	0.24
peptidylprolyl isomerase A (cyclophilin A)-like 4E [Homo sapiens]	4.58	1.90	2.68	2.49	1.93
PREDICTED: mitogen-activated protein kinase 12 isoform X1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	1.31	1.90	2.68	2.33	1.63
PREDICTED: myosin regulatory light chain 12B-like	0.83	0.87	0.89	0.88	0.95

[Homo sapiens]					
PREDICTED: small ubiquitin-related modifier 2-like [Homo sapiens]	1.64	0.99	1.22	1.47	0.99
PREDICTED: NAD kinase isoform X2 [Homo sapiens]	2.27	0.97	2.29	1.22	2.16
PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform isoform X2 [Homo sapiens]	2.02	0.76	2.47	1.54	0.89
PREDICTED: protein LZIC isoform X2 [Homo sapiens]	1.89	0.79	0.56	0.33	0.58
PREDICTED: protein LZIC isoform X4 [Homo sapiens]	1.89	0.79	0.56	0.33	0.58
PREDICTED: voltage-gated potassium channel subunit beta-2 isoform X2 [Homo sapiens]	0.98	2.18	1.95	2.29	1.79
PREDICTED: voltage-gated potassium channel subunit beta-2 isoform X4 [Homo sapiens]	0.88	1.98	1.91	2.37	1.86
PREDICTED: acyl-protein thioesterase 2 isoform X1 [Homo sapiens]	0.54	0.96	0.63	0.73	1.61
PREDICTED: protein 4.1 isoform X1 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X5 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X8 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X11 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X12 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X13 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X15 [Homo sapiens]	24.91	0.94	0.88	0.46	0.92
PREDICTED: protein 4.1 isoform X16 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X17 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X18 [Homo sapiens]	0.57	0.68	0.18	0.08	0.33
PREDICTED: protein 4.1 isoform X20 [Homo sapiens]	24.91	0.94	0.88	0.46	0.92
PREDICTED: protein 4.1 isoform X21 [Homo sapiens]	24.91	0.94	0.88	0.46	0.92
PREDICTED: protein 4.1 isoform X22 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X5 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X3 [Homo sapiens]	0.54	0.68	0.66	1.20	1.42
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X5 [Homo sapiens]	0.54	0.68	0.66	1.20	1.42
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X8 [Homo sapiens]	0.45	0.65	0.67	1.21	1.54
PREDICTED: PITH domain-containing protein 1 isoform X1 [Homo sapiens]	8.66	2.20	0.94	0.81	1.42
PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X1 [Homo sapiens]	0.88	0.91	1.40	2.30	1.59
PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X2 [Homo sapiens]	0.88	0.91	1.40	2.30	1.59
PREDICTED: centrosomal protein of 85 kDa isoform X1 [Homo sapiens]	732.97	0.96	3.92	0.88	2.50
PREDICTED: EF-hand domain-containing protein D2 isoform X1 [Homo sapiens]	0.57	1.96	1.37	1.68	1.42
PREDICTED: CTP synthase 1 isoform X2 [Homo sapiens]	1.54	0.93	0.70	0.99	1.21
PREDICTED: epidermal growth factor receptor substrate 15 isoform X2 [Homo sapiens]	0.62	1.40	1.37	1.35	0.88
PREDICTED: AMP deaminase 2 isoform X1 [Homo sapiens]	1.34	0.88	0.66	0.75	0.91
PREDICTED: glutamate--cysteine ligase regulatory subunit isoform X1 [Homo sapiens]	0.80	0.97	0.55	0.35	0.64
PREDICTED: neuron-specific calcium-binding protein hippocalcin isoform X1 [Homo sapiens]	4.07	1.19	1.34	1.98	1.45
PREDICTED: bcl-2-like protein 15 isoform X1 [Homo sapiens]	0.64	1.51	1.30	1.43	0.92
PREDICTED: nuclease-sensitive element-binding protein 1 isoform X1 [Homo sapiens]	3.86	1.69	5.56	6.36	4.53

PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X1 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X2 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X3 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X4 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X5 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X6 [Homo sapiens]	1.31	0.83	1.27	1.52	0.98
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X7 [Homo sapiens]	1.31	0.83	1.27	1.52	0.98
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X8 [Homo sapiens]	1.31	0.83	1.27	1.52	0.98
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X9 [Homo sapiens]	1.31	0.83	1.27	1.52	0.98
PREDICTED: splicing factor, proline- and glutamine-rich isoform X2 [Homo sapiens]	1.00	0.93	1.00	1.47	0.94
PREDICTED: splicing factor, proline- and glutamine-rich isoform X6 [Homo sapiens]	1.00	0.93	1.00	1.47	0.94
PREDICTED: complement component C8 beta chain isoform X1 [Homo sapiens]	0.33	2.08	0.53	0.31	0.52
PREDICTED: far upstream element-binding protein 1 isoform X1 [Homo sapiens]	0.77	0.77	0.98	0.82	2.60
PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	0.62	0.64	0.40	0.24	0.50
PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sapiens]	0.62	0.64	0.40	0.24	0.50
PREDICTED: farnesyl pyrophosphate synthase isoform X1 [Homo sapiens]	4.38	1.17	3.59	5.56	2.71
PREDICTED: rho GTPase-activating protein 30 isoform X1 [Homo sapiens]	0.10	1.17	2.29	1.78	0.98
PREDICTED: rho GTPase-activating protein 30 isoform X2 [Homo sapiens]	0.10	1.17	2.29	1.78	0.98
PREDICTED: dynamin-3 isoform X1 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: dynamin-3 isoform X2 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: dynamin-3 isoform X3 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: dynamin-3 isoform X4 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: dynamin-3 isoform X6 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: complement factor H-related protein 2 isoform X1 [Homo sapiens]	0.41	2.20	0.77	0.25	0.70
PREDICTED: gamma-interferon-inducible protein 16 isoform X1 [Homo sapiens]	0.35	0.64	0.33	0.30	0.44
PREDICTED: antithrombin-III isoform X1 [Homo sapiens]	0.43	0.82	0.40	0.22	0.61
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X3 [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
PREDICTED: neutrophil cytosol factor 2 isoform X1 [Homo sapiens]	0.75	0.71	0.77	0.87	0.80
PREDICTED: nitrilase homolog 1 isoform X1 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
PREDICTED: nitrilase homolog 1 isoform X2 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
PREDICTED: nitrilase homolog 1 isoform X3 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
PREDICTED: ubiquitin-fold modifier-conjugating enzyme 1 isoform X1 [Homo sapiens]	2.49	1.62	1.68	0.94	0.96
PREDICTED: pyruvate kinase PKLR isoform X1 [Homo sapiens]	0.43	0.87	1.78	1.72	1.27
PREDICTED: aminopeptidase B isoform X1 [Homo sapiens]	1.21	0.88	1.28	1.65	0.94
PREDICTED: aminopeptidase B isoform X2 [Homo sapiens]	1.21	0.88	1.28	1.65	0.94

PREDICTED: aminopeptidase B isoform X4 [Homo sapiens]	2.79	0.85	1.22	1.53	0.94
PREDICTED: nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 isoform X1 [Homo sapiens]	1.51	1.21	2.32	4.27	1.94
PREDICTED: sorting nexin-27 isoform X1 [Homo sapiens]	0.75	0.94	0.93	1.26	0.98
PREDICTED: sorting nexin-27 isoform X2 [Homo sapiens]	2.27	0.93	0.68	0.80	0.76
PREDICTED: sorting nexin-27 isoform X3 [Homo sapiens]	2.27	0.93	0.68	0.80	0.76
PREDICTED: sorting nexin-27 isoform X4 [Homo sapiens]	2.27	0.93	0.68	0.80	0.76
PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member E isoform X1 [Homo sapiens]	0.95	0.80	0.83	1.97	0.90
PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member E isoform X2 [Homo sapiens]	0.95	0.80	0.81	0.98	0.94
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X1 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X2 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X3 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X4 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X6 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X9 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: CD5 antigen-like isoform X1 [Homo sapiens]	0.46	0.97	0.40	0.23	0.65
PREDICTED: capZ-interacting protein isoform X1 [Homo sapiens]	0.19	0.70	1.19	1.28	0.76
PREDICTED: zinc finger CCCH domain-containing protein 11A isoform X5 [Homo sapiens]		0.43	0.51	1.37	0.50
PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1 isoform X1 [Homo sapiens]	2.54	0.93	1.24	1.17	1.21
PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1 isoform X8 [Homo sapiens]	1.44	0.79	0.78	0.68	0.81
PREDICTED: complement receptor type 1 isoform X1 [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
PREDICTED: BRO1 domain-containing protein BROX isoform X1 [Homo sapiens]	1.76	1.00	1.27	1.21	0.92
PREDICTED: BRO1 domain-containing protein BROX isoform X2 [Homo sapiens]	1.61	0.88	0.94	0.79	0.90
PREDICTED: BRO1 domain-containing protein BROX isoform X5 [Homo sapiens]	1.76	1.00	1.27	1.21	0.92
PREDICTED: lamin-B receptor isoform X1 [Homo sapiens]	0.46	0.89	0.96	2.49	1.30
PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo sapiens]	0.54	1.22	0.69	0.50	0.93
PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sapiens]	0.56	1.27	0.73	0.45	0.96
PREDICTED: C4b-binding protein beta chain isoform X2 [Homo sapiens]	0.67	1.30	0.61	0.38	0.81
PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]	0.88	1.51	0.61	0.46	0.83
PREDICTED: MAP kinase-activated protein kinase 2 isoform X1 [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
PREDICTED: protein disulfide-isomerase A6 isoform X3 [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
PREDICTED: hippocalcin-like protein 1 isoform X2 [Homo sapiens]	4.07	1.19	1.34	1.98	1.45
PREDICTED: rho-associated protein kinase 2 isoform X1 [Homo sapiens]	0.95	0.81	0.58	0.38	0.57

PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]	0.57	2.39	0.45	0.23	0.63
PREDICTED: echinoderm microtubule-associated protein-like 4 isoform X1 [Homo sapiens]	1.28	1.53	1.87	1.25	1.54
PREDICTED: echinoderm microtubule-associated protein-like 4 isoform X2 [Homo sapiens]	1.28	1.53	1.87	1.25	1.54
PREDICTED: hexokinase-2 isoform X1 [Homo sapiens]	4.74	1.62	1.31	1.25	1.17
PREDICTED: V-type proton ATPase subunit B, kidney isoform isoform X1 [Homo sapiens]	2.49	0.95	0.90	0.65	0.84
PREDICTED: N-acetyl-D-glucosamine kinase isoform X1 [Homo sapiens]	0.64	0.87	0.85	0.83	1.18
PREDICTED: reticulon-4 isoform X1 [Homo sapiens]	7.95	1.51	1.30	1.96	0.90
PREDICTED: ras-related protein Rab-1A isoform X1 [Homo sapiens]	0.88	1.30	2.07	2.75	1.25
PREDICTED: serine/arginine-rich splicing factor 7 isoform X1 [Homo sapiens]	1.68	0.67	0.45	0.43	0.66
PREDICTED: serine/arginine-rich splicing factor 7 isoform X2 [Homo sapiens]	1.68	0.67	0.45	0.43	0.66
PREDICTED: serine/arginine-rich splicing factor 7 isoform X3 [Homo sapiens]	1.68	0.67	0.45	0.43	0.66
PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	1.18	1.24	1.27	1.56	1.26
PREDICTED: UTP--glucose-1-phosphate uridylyltransferase isoform X2 [Homo sapiens]	2.38	1.62	1.30	1.43	1.61
PREDICTED: exportin-1 isoform X1 [Homo sapiens]	4.16	1.26	0.90	1.43	1.61
PREDICTED: exportin-1 isoform X3 [Homo sapiens]	5.15	1.96	0.77	0.95	0.92
PREDICTED: macrophage-capping protein isoform X1 [Homo sapiens]	0.45	1.73	1.44	1.57	1.24
PREDICTED: dysferlin isoform X1 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
PREDICTED: dysferlin isoform X2 [Homo sapiens]	1.64	1.69	1.43	0.69	1.94
PREDICTED: rho GTPase-activating protein 25 isoform X1 [Homo sapiens]	0.64	1.00	1.43	0.98	0.94
PREDICTED: rho GTPase-activating protein 25 isoform X2 [Homo sapiens]	0.56	0.95	1.23	1.74	1.21
PREDICTED: beta-centractin isoform X1 [Homo sapiens]	3.79	1.41	1.97	2.49	1.35
PREDICTED: eukaryotic translation initiation factor 5B isoform X1 [Homo sapiens]	1.96	1.28	1.00	0.89	0.94
PREDICTED: myc box-dependent-interacting protein 1 isoform X1 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X2 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X3 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X4 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X5 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X6 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X7 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: rho GTPase-activating protein 15 isoform X1 [Homo sapiens]	1.18	2.45	1.72	2.14	1.28
PREDICTED: vitamin K-dependent protein C isoform X1 [Homo sapiens]	0.43	0.43	0.30	0.13	0.23
PREDICTED: vitamin K-dependent protein C isoform X2 [Homo sapiens]	0.43	0.43	0.30	0.13	0.23
PREDICTED: vitamin K-dependent protein C isoform X3 [Homo sapiens]	0.43	0.43	0.30	0.13	0.23
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X2 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X3 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98

PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X4 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X7 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X2 [Homo sapiens]	1.18	0.79	0.95	1.98	1.88
PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X3 [Homo sapiens]	0.77	0.97	1.34	1.75	1.34
PREDICTED: fibronectin isoform X1 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X2 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X3 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X4 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X5 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X6 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X7 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X8 [Homo sapiens]	0.67	1.44	0.70	0.74	1.38
PREDICTED: fibronectin isoform X9 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X10 [Homo sapiens]	0.67	1.44	0.70	0.74	1.38
PREDICTED: fibronectin isoform X11 [Homo sapiens]	0.67	1.41	0.70	0.73	1.37
PREDICTED: fibronectin isoform X12 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X13 [Homo sapiens]	0.67	1.44	0.70	0.74	1.38
PREDICTED: fibronectin isoform X14 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X15 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X16 [Homo sapiens]	0.67	1.44	0.70	0.75	1.38
PREDICTED: fibronectin isoform X17 [Homo sapiens]	0.67	1.42	0.70	0.74	1.37
PREDICTED: fibronectin isoform X18 [Homo sapiens]	0.67	1.44	0.70	0.74	1.38
PREDICTED: fibronectin isoform X19 [Homo sapiens]	0.67	1.44	0.70	0.75	1.38
PREDICTED: fibronectin isoform X20 [Homo sapiens]	0.67	1.44	0.70	0.75	1.38
PREDICTED: fibronectin isoform X21 [Homo sapiens]	0.67	1.44	0.70	0.75	1.38
PREDICTED: splicing factor 3B subunit 1 isoform X1 [Homo sapiens]	0.91	0.80	0.41	0.27	0.53
PREDICTED: grancalcin isoform X1 [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
PREDICTED: mannose-1-phosphate guanylttransferase alpha isoform X3 [Homo sapiens]	1.64	0.95	1.51	1.72	1.24
PREDICTED: peptidyl-prolyl cis-trans isomerase-like 3 isoform X2 [Homo sapiens]	3.34	0.97	1.43	1.98	0.95
PREDICTED: dedicator of cytokinesis protein 10 isoform X1 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X2 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: pre-mRNA-processing factor 40 homolog A isoform X5 [Homo sapiens]	0.33	0.92	1.46	2.49	1.57
PREDICTED: tubulin alpha-4A chain isoform X1 [Homo sapiens]	0.41	0.88	0.93	0.67	1.81
PREDICTED: X-ray repair cross-complementing protein 5 isoform X1 [Homo sapiens]	0.80	0.97	1.30	1.26	1.94
PREDICTED: X-ray repair cross-complementing protein 5 isoform X2 [Homo sapiens]	0.91	0.95	1.43	1.98	1.35
PREDICTED: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform X1 [Homo sapiens]	0.26	1.96	0.88	1.37	0.76
PREDICTED: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform X2 [Homo sapiens]	0.26	1.96	0.88	1.37	0.76
PREDICTED: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform X3 [Homo sapiens]	0.26	1.96	0.88	1.37	0.76
PREDICTED: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform X4 [Homo sapiens]	0.26	1.96	0.88	1.37	0.76

sapiens]					
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X1 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X3 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X4 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X5 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X7 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X9 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X10 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: collagen alpha-3(VI) chain isoform X1 [Homo sapiens]	2.11	1.59	0.52	0.32	0.82
PREDICTED: collagen alpha-3(VI) chain isoform X2 [Homo sapiens]	2.15	1.79	0.52	0.32	0.90
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X1 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X2 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X3 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X4 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X5 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X6 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X7 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X8 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X9 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X10 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X11 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X12 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X13 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X14 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X15 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X16 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X17 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X18 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X19 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X20 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X21 [Homo sapiens]	0.54	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X22 [Homo sapiens]	0.54	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X23 [Homo sapiens]	0.57	1.62	1.21	2.51	0.74
PREDICTED: leucine-rich repeat flightless-interacting	0.57	1.62	1.21	2.51	0.74

protein 1 isoform X24 [Homo sapiens]					
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X25 [Homo sapiens]	0.57	1.62	1.21	2.51	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X26 [Homo sapiens]	3.70	2.59	0.75	0.57	0.88
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X27 [Homo sapiens]	3.70	2.59	0.75	0.57	0.88
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X28 [Homo sapiens]	3.70	2.59	0.75	0.57	0.88
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X29 [Homo sapiens]	1.31	2.20	1.90	1.28	2.08
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X30 [Homo sapiens]	0.91	2.71	1.60	1.21	2.34
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X31 [Homo sapiens]	0.66	2.59	1.55	2.39	1.37
PREDICTED: ubiquitin-like modifier-activating enzyme ATG7 isoform X4 [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
PREDICTED: filamin-B isoform X1 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
PREDICTED: filamin-B isoform X2 [Homo sapiens]	0.80	0.83	0.78	0.73	0.92
PREDICTED: filamin-B isoform X5 [Homo sapiens]	0.69	0.84	0.81	0.75	0.93
PREDICTED: filamin-B isoform X6 [Homo sapiens]	0.69	0.84	0.81	0.75	0.93
PREDICTED: neurobeachin-like protein 2 isoform X3 [Homo sapiens]	1.64	0.74	0.56	0.64	0.61
PREDICTED: neurobeachin-like protein 2 isoform X4 [Homo sapiens]	0.77	0.78	0.81	1.65	0.70
PREDICTED: acylamino-acid-releasing enzyme isoform X1 [Homo sapiens]	5.61	2.08	1.34	2.01	1.18
PREDICTED: acylamino-acid-releasing enzyme isoform X2 [Homo sapiens]	8.48	2.08	1.83	1.80	1.54
PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X1 [Homo sapiens]	0.67	1.26	0.80	0.44	2.34
PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit isoform X2 [Homo sapiens]		0.41	1.60	1.23	1.91
PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit isoform X3 [Homo sapiens]		0.41	1.60	1.23	1.91
PREDICTED: protein SEC13 homolog isoform X1 [Homo sapiens]	1.00	1.24	1.29	1.68	1.30
PREDICTED: protein SEC13 homolog isoform X2 [Homo sapiens]	1.31	1.19	0.79	0.82	0.89
PREDICTED: protein SEC13 homolog isoform X3 [Homo sapiens]	1.31	1.19	0.79	0.82	0.89
PREDICTED: protein-glutamine gamma-glutamyltransferase 4 isoform X1 [Homo sapiens]	0.14	0.70	0.32	0.22	3.48
PREDICTED: tetranectin isoform X1 [Homo sapiens]	0.56	0.78	0.29	0.18	0.32
PREDICTED: DNA topoisomerase 2-beta isoform X1 [Homo sapiens]	0.45	1.19	1.44	5.02	1.64
PREDICTED: ubiquitin-like modifier-activating enzyme 7 isoform X2 [Homo sapiens]	0.39	0.88	0.88	0.89	1.28
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X1 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X13 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X14 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X20 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X1 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X2 [Homo sapiens]	0.64	1.35	0.71	0.68	0.82
PREDICTED: serine/threonine-protein kinase OSR1 isoform X1 [Homo sapiens]	3.39	0.97	2.26	0.75	0.88
PREDICTED: copine-4 isoform X3 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: dnaJ homolog subfamily C member 13	2.66	0.85	1.21	1.81	1.48

isoform X1 [Homo sapiens]

PREDICTED: fetuin-B isoform X3 [Homo sapiens]	0.31	0.71	0.38	0.13	0.50
PREDICTED: fetuin-B isoform X4 [Homo sapiens]	0.31	0.71	0.41	0.24	0.53
PREDICTED: histidine-rich glycoprotein isoform X1 [Homo sapiens]	0.43	0.73	0.37	0.22	0.61
PREDICTED: DCN1-like protein 1 isoform X2 [Homo sapiens]	12.38	1.34	1.87	2.28	1.34
PREDICTED: vitamin K-dependent protein S isoform X1 [Homo sapiens]	0.67	2.59	0.65	0.37	0.96
PREDICTED: cholinesterase isoform X1 [Homo sapiens]	0.91	0.85	0.39	0.21	0.52
PREDICTED: voltage-gated potassium channel subunit beta-1 isoform X1 [Homo sapiens]	1.24	2.21	1.95	1.41	2.05
PREDICTED: voltage-gated potassium channel subunit beta-1 isoform X2 [Homo sapiens]	1.24	2.21	1.95	1.41	2.05
PREDICTED: ruvB-like 1 isoform X1 [Homo sapiens]	2.66	0.91	1.72	1.22	0.90
PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform X1 [Homo sapiens]	0.28	0.93	1.21	2.77	0.84
PREDICTED: alpha-adducin isoform X1 [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
PREDICTED: alpha-adducin isoform X3 [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
PREDICTED: alpha-adducin isoform X4 [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
PREDICTED: alpha-adducin isoform X5 [Homo sapiens]	0.64	1.00	0.61	0.42	0.69
PREDICTED: protein phosphatase 2, regulatory subunit B, gamma isoform X3 [Homo sapiens]	1.37	0.79	0.55	0.39	0.64
PREDICTED: protein phosphatase 2, regulatory subunit B, gamma isoform X4 [Homo sapiens]	1.37	0.79	0.55	0.39	0.64
PREDICTED: ADP-ribosyl cyclase 2 isoform X1 [Homo sapiens]	0.66	1.98	1.27	0.96	1.23
PREDICTED: ADP-ribosyl cyclase 2 isoform X2 [Homo sapiens]	0.66	1.98	1.27	0.96	1.23
PREDICTED: ADP-ribosyl cyclase 2 isoform X3 [Homo sapiens]	0.66	1.98	1.27	0.96	1.23
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X1 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X2 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X3 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X4 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X5 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X6 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X7 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X8 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X9 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X10 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X13 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X14 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X15 [Homo sapiens]	0.75	0.94	0.49	0.31	0.75
PREDICTED: sulfotransferase family cytosolic 1B member 1 isoform X1 [Homo sapiens]	0.33	0.70	0.75	0.77	0.69
PREDICTED: sulfotransferase family cytosolic 1B	0.33	0.70	0.75	0.77	0.69

member 1 isoform X3 [Homo sapiens]					
PREDICTED: MOB kinase activator 1B isoform X1 [Homo sapiens]	1.71	0.96	1.29	1.44	0.94
PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	0.33	1.30	0.69	0.30	0.81
PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	0.33	1.30	0.69	0.30	0.81
PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	0.33	1.30	0.69	0.30	0.81
PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	0.33	1.30	0.71	0.41	0.96
PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	0.46	0.93	0.50	0.28	0.64
PREDICTED: long-chain-fatty-acid--CoA ligase 1 isoform X1 [Homo sapiens]	0.69	1.35	1.60	1.56	0.82
PREDICTED: long-chain-fatty-acid--CoA ligase 1 isoform X2 [Homo sapiens]	0.69	1.35	1.60	1.56	0.82
PREDICTED: histone H2A.Z isoform X1 [Homo sapiens]	0.35	5.03	0.79	0.55	0.82
PREDICTED: hydroxyacyl-coenzyme A dehydrogenase, mitochondrial isoform X1 [Homo sapiens]	0.64	1.53	1.96	0.58	0.88
PREDICTED: complement factor I isoform X1 [Homo sapiens]	0.43	1.51	0.58	0.31	0.69
PREDICTED: complement factor I isoform X2 [Homo sapiens]	0.43	1.51	0.58	0.31	0.69
PREDICTED: plasma kallikrein isoform X1 [Homo sapiens]	0.33	0.62	0.29	0.18	0.43
PREDICTED: nuclear factor NF-kappa-B p105 subunit isoform X1 [Homo sapiens]	1.96	0.55	0.40	0.24	0.44
PREDICTED: septin-11 isoform X1 [Homo sapiens]	1.24	0.92	1.34	1.18	1.74
PREDICTED: septin-11 isoform X2 [Homo sapiens]	1.24	0.92	1.34	1.18	1.74
PREDICTED: septin-11 isoform X3 [Homo sapiens]	1.24	0.92	1.34	1.18	1.74
PREDICTED: mitogen-activated protein kinase 10 isoform X2 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: mitogen-activated protein kinase 10 isoform X4 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: mitogen-activated protein kinase 10 isoform X9 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: ubiquitin-conjugating enzyme E2 D3 isoform X6 [Homo sapiens]	1.31	0.85	1.21	1.24	0.96
PREDICTED: N-alpha-acetyltransferase 15, NatA auxiliary subunit isoform X1 [Homo sapiens]	1.18	1.40	0.80	0.76	0.71
PREDICTED: myosin regulatory light chain 12B-like [Homo sapiens]	0.83	0.87	0.89	0.88	0.95
PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]	3.12	2.45	0.70	0.43	0.79
PREDICTED: complement component C6 isoform X1 [Homo sapiens]	0.33	1.90	0.64	0.33	0.67
PREDICTED: complement component C6 isoform X2 [Homo sapiens]	0.33	1.90	0.64	0.33	0.67
PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X1 [Homo sapiens]	1.18	1.30	1.54	1.57	0.96
PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X3 [Homo sapiens]	1.18	1.30	1.54	1.57	0.96
PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X5 [Homo sapiens]	0.64	1.30	1.21	1.65	0.96
PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X6 [Homo sapiens]	1.21	0.84	0.90	1.37	0.96
PREDICTED: transportin-1 isoform X2 [Homo sapiens]	2.38	0.68	1.23	2.81	1.48
PREDICTED: probable ATP-dependent RNA helicase DDX4 isoform X1 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
PREDICTED: probable ATP-dependent RNA helicase DDX4 isoform X3 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
PREDICTED: polycystic kidney disease 2-like 2 protein isoform X1 [Homo sapiens]	0.19	0.61	0.39	0.20	0.67

PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]	2.38	1.19	0.88	0.62	0.75
PREDICTED: core histone macro-H2A.1 isoform X5 [Homo sapiens]	0.88	1.65	0.90	0.45	0.75
PREDICTED: core histone macro-H2A.1 isoform X6 [Homo sapiens]	0.88	1.65	0.90	0.45	0.75
PREDICTED: probable ATP-dependent RNA helicase DDX46 isoform X1 [Homo sapiens]	0.95	0.78	0.96	2.21	0.88
PREDICTED: glucosamine-6-phosphate isomerase 1 isoform X1 [Homo sapiens]	1.79	0.87	0.78	0.51	0.81
PREDICTED: protein diaphanous homolog 1 isoform X1 [Homo sapiens]	1.21	0.93	1.43	2.51	2.30
PREDICTED: histidine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	2.17	1.39	2.26	4.80	1.77
PREDICTED: annexin A6 isoform X2 [Homo sapiens]	0.91	2.01	1.62	1.79	1.63
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X2 [Homo sapiens]	0.18	0.68	0.21	0.08	0.41
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X6 [Homo sapiens]	0.18	0.68	0.21	0.08	0.41
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X7 [Homo sapiens]	0.18	0.68	0.21	0.08	0.41
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X10 [Homo sapiens]	0.18	0.68	0.21	0.08	0.41
PREDICTED: prefoldin subunit 1 isoform X1 [Homo sapiens]	0.95	1.53	1.46	1.22	1.45
PREDICTED: dedicator of cytokinesis protein 2 isoform X1 [Homo sapiens]	0.69	0.99	2.69	1.77	2.45
PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X1 [Homo sapiens]	4.84	1.69	2.26	3.89	1.47
PREDICTED: nucleophosmin isoform X2 [Homo sapiens]	0.75	1.30	1.41	0.88	1.38
PREDICTED: mitogen-activated protein kinase 9 isoform X1 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: arginine--tRNA ligase, cytoplasmic isoform X2 [Homo sapiens]	2.33	0.79	0.70	0.56	0.80
PREDICTED: docking protein 3 isoform X3 [Homo sapiens]	1.34	0.89	0.67	0.89	0.75
PREDICTED: docking protein 3 isoform X5 [Homo sapiens]	0.91	0.80	0.48	0.52	0.68
PREDICTED: protein canopy homolog 3 isoform X1 [Homo sapiens]	0.77	1.30	0.98	0.57	0.82
PREDICTED: protein canopy homolog 3 isoform X3 [Homo sapiens]	1.28	2.32	0.78	0.46	0.83
PREDICTED: protein canopy homolog 3 isoform X4 [Homo sapiens]	1.28	2.32	0.78	0.46	0.83
PREDICTED: peptidase inhibitor 16 isoform X3 [Homo sapiens]	0.16	1.58	0.39	0.27	0.62
PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]	0.46	0.58	0.23	0.19	0.46
PREDICTED: histone H2B type 1-D isoform X1 [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
PREDICTED: heat shock 70 kDa protein 1-like isoform X1 [Homo sapiens]	2.79	1.25	1.30	1.24	2.68
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	2.79	1.25	1.30	1.24	2.68
PREDICTED: heat shock protein HSP 90-beta isoform X1 [Homo sapiens]	1.21	1.62	1.43	1.33	0.93
PREDICTED: ribosylidihydronicotinamide dehydrogenase [quinone] isoform X4 [Homo sapiens]	1.37	2.20	1.44	1.60	1.21
PREDICTED: serpin B6 isoform X1 [Homo sapiens]	1.54	2.71	1.19	0.96	2.68
PREDICTED: serpin B6 isoform X3 [Homo sapiens]	1.54	2.71	1.19	0.96	2.68

PREDICTED: serpin B9 isoform X1 [Homo sapiens]	1.00	1.30	1.18	1.33	1.82
PREDICTED: copine-5 isoform X1 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: copine-5 isoform X2 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: copine-5 isoform X6 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: protein DEK isoform X2 [Homo sapiens]	1.21	0.81	0.54	2.09	1.82
PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform X1 [Homo sapiens]	4.58	0.80	0.87	0.94	0.90
PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform X2 [Homo sapiens]	1.41	2.08	2.69	1.64	1.17
PREDICTED: SAM and SH3 domain-containing protein 1 isoform X1 [Homo sapiens]	0.52	0.91	0.79	0.85	0.83
PREDICTED: SAM and SH3 domain-containing protein 1 isoform X2 [Homo sapiens]	0.52	0.91	0.79	0.85	0.83
PREDICTED: acetyl-CoA acetyltransferase, cytosolic isoform X1 [Homo sapiens]	15.35	0.91	1.55	1.48	1.38
PREDICTED: prolyl endopeptidase isoform X1 [Homo sapiens]	1.41	0.85	0.84	1.19	1.61
PREDICTED: ribonuclease T2 isoform X1 [Homo sapiens]	0.95	2.09	2.38	2.16	1.94
PREDICTED: ribonuclease T2 isoform X2 [Homo sapiens]	0.57	1.34	1.29	1.18	1.61
PREDICTED: sorting nexin-3 isoform X2 [Homo sapiens]	5.15	1.62	1.57	3.41	2.34
PREDICTED: chromobox protein homolog 3 isoform X2 [Homo sapiens]	2.00	0.89	0.84	1.44	1.28
PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X1 [Homo sapiens]	0.80	0.95	1.30	1.61	1.23
PREDICTED: peptidyl-prolyl cis-trans isomerase A isoform X1 [Homo sapiens]	2.66	1.38	1.73	2.02	1.80
PREDICTED: engulfment and cell motility protein 1 isoform X1 [Homo sapiens]	0.31	0.93	0.97	1.64	0.96
PREDICTED: semaphorin-3C isoform X2 [Homo sapiens]	0.31	0.56	0.21	0.09	0.32
PREDICTED: beta-glucuronidase isoform X1 [Homo sapiens]	0.75	1.82	1.64	0.96	2.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X1 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X2 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: exocyst complex component 4 isoform X4 [Homo sapiens]	0.25	0.65	0.27	0.15	0.65
PREDICTED: GTPase IMAP family member 4 isoform X1 [Homo sapiens]	0.62	0.57	0.55	0.63	0.67
PREDICTED: single-stranded DNA-binding protein, mitochondrial isoform X1 [Homo sapiens]	0.66	1.51	0.71	0.53	0.78
PREDICTED: zyxin isoform X1 [Homo sapiens]	0.67	1.62	0.77	1.51	0.68
PREDICTED: zyxin isoform X2 [Homo sapiens]	0.67	1.62	0.77	1.51	0.68
PREDICTED: kelch repeat and BTB domain-containing protein 11 isoform X1 [Homo sapiens]	0.33	0.93	0.98	2.13	0.93
PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X1 [Homo sapiens]	3.56	1.47	2.49	4.11	1.71
PREDICTED: protein-tyrosine kinase 2-beta isoform X1 [Homo sapiens]	0.23	0.91	2.09	2.25	1.28
PREDICTED: protein-tyrosine kinase 2-beta isoform X2 [Homo sapiens]	0.23	0.91	2.09	2.25	1.28
PREDICTED: ankyrin-1 isoform X1 [Homo sapiens]	1.31	0.66	0.37	0.23	0.58
PREDICTED: acid ceramidase isoform X1 [Homo sapiens]	1.61	2.20	2.60	2.35	2.40
PREDICTED: piwi-like protein 2 isoform X1 [Homo sapiens]	7.02	2.20	0.74	0.43	0.64
PREDICTED: piwi-like protein 2 isoform X2 [Homo sapiens]	7.02	2.20	0.74	0.43	0.64
PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform isoform X1	1.64	0.89	2.26	1.51	0.99

[Homo sapiens]

PREDICTED: serine/threonine-protein phosphatase 2A
55 kDa regulatory subunit B alpha isoform isoform X2
[Homo sapiens]

1.34 0.89 1.51 0.94 0.94

PREDICTED: stathmin-4 isoform X1 [Homo sapiens]

0.77 0.94 3.60 7.80 1.58

PREDICTED: stathmin-4 isoform X4 [Homo sapiens]

0.77 0.94 3.60 7.80 1.58

PREDICTED: acyl-protein thioesterase 1 isoform X1
[Homo sapiens]

0.80 0.79 0.82 0.99 0.90

PREDICTED: stathmin-2 isoform X2 [Homo sapiens]

1.34 0.93 1.51 2.22 1.29

PREDICTED: RNA-binding Raly-like protein isoform X1
[Homo sapiens]

2.79 0.79 1.48 4.80 1.35

PREDICTED: tyrosine-protein kinase Lyn isoform X2
[Homo sapiens]

2.79 1.73 2.76 1.55 0.90

PREDICTED: syntenin-1 isoform X1 [Homo sapiens]

0.52 0.77 0.31 0.13 0.42

PREDICTED: ubiquitin-conjugating enzyme E2 variant
2 isoform X1 [Homo sapiens]

8.90 1.26 1.36 1.27 1.29

PREDICTED: leucine-rich repeat and coiled-coil
domain-containing protein 1 isoform X1 [Homo
sapiens]

3.70 1.75 1.98 2.19 2.11

PREDICTED: leucine-rich repeat and coiled-coil
domain-containing protein 1 isoform X2 [Homo
sapiens]

3.70 1.75 1.98 2.19 2.11

PREDICTED: leucine-rich repeat and coiled-coil
domain-containing protein 1 isoform X3 [Homo
sapiens]

3.70 1.75 1.98 2.19 2.11

PREDICTED: leucine-rich repeat and coiled-coil
domain-containing protein 1 isoform X5 [Homo
sapiens]

3.70 1.75 1.98 2.19 2.11

PREDICTED: leucine-rich repeat and coiled-coil
domain-containing protein 1 isoform X6 [Homo
sapiens]

3.70 1.75 1.98 2.19 2.11

PREDICTED: elongation factor 1-delta isoform X1
[Homo sapiens]

0.25 0.83 0.71 0.44 0.67

PREDICTED: protein FAM49B isoform X4 [Homo
sapiens]

0.46 0.98 0.82 0.98 1.61

PREDICTED: plectin isoform X1 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X2 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X3 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X4 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X5 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X6 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X7 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X8 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: plectin isoform X9 [Homo sapiens]

0.75 0.96 0.90 1.66 0.68

PREDICTED: GDP-L-fucose synthase isoform X1
[Homo sapiens]

12.66 0.98 1.87 0.90 2.01

PREDICTED: GDP-L-fucose synthase isoform X2
[Homo sapiens]

12.66 0.98 1.87 0.90 2.01

PREDICTED: GDP-L-fucose synthase isoform X3
[Homo sapiens]

12.66 0.98 1.87 0.90 2.01

PREDICTED: 14-3-3 protein zeta/delta isoform X1
[Homo sapiens]

1.18 1.73 1.55 2.06 1.36

PREDICTED: 14-3-3 protein zeta/delta isoform X3
[Homo sapiens]

1.18 1.73 1.55 2.06 1.36

PREDICTED: WASH complex subunit strumpellin
isoform X1 [Homo sapiens]

1.61 1.44 0.71 0.53 0.90

PREDICTED: PC4 and SFRS1-interacting protein
isoform X1 [Homo sapiens]

0.67 1.22 2.79 4.74 1.52

PREDICTED: PC4 and SFRS1-interacting protein
isoform X3 [Homo sapiens]

0.67 1.22 2.79 4.74 1.52

PREDICTED: PC4 and SFRS1-interacting protein
isoform X4 [Homo sapiens]

0.67 1.22 2.79 4.74 1.52

PREDICTED: trypsin-3 isoform X1 [Homo sapiens]	1.82	0.51	0.30	0.15	0.32
PREDICTED: talin-1 isoform X1 [Homo sapiens]	1.24	0.97	1.21	1.51	2.08
PREDICTED: tropomyosin beta chain isoform X3 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
PREDICTED: tropomyosin beta chain isoform X5 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
PREDICTED: tropomyosin beta chain isoform X6 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
PREDICTED: tropomyosin beta chain isoform X7 [Homo sapiens]	4.74	0.73	0.84	0.57	0.68
PREDICTED: dynamin-1 isoform X1 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
PREDICTED: dynamin-1 isoform X2 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
PREDICTED: adenylate kinase isoenzyme 1 isoform X1 [Homo sapiens]	192.45	0.88	0.82	0.38	0.92
PREDICTED: adenylate kinase isoenzyme 1 isoform X3 [Homo sapiens]	192.45	0.88	0.82	0.38	0.92
PREDICTED: delta-aminolevulinic acid dehydratase isoform X1 [Homo sapiens]	12.66	0.94	0.66	0.49	0.74
PREDICTED: formin-binding protein 1 isoform X1 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X2 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X3 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X4 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X5 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X6 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X7 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X8 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X9 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X10 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X11 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X12 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X13 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X14 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X15 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X16 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X17 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X18 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X19 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: ubiquitin-1 isoform X1 [Homo sapiens]	1.28	1.24	0.91	0.87	1.20
PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X5 [Homo sapiens]	1.64	0.79	1.43	2.16	2.30
PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]	1.64	0.79	1.43	2.16	2.30
PREDICTED: tenascin isoform X1 [Homo sapiens]	1.54	4.13	0.95	0.61	1.42

PREDICTED: tenascin isoform X2 [Homo sapiens]	1.34	4.33	0.98	0.62	1.94
PREDICTED: tenascin isoform X3 [Homo sapiens]	1.47	4.07	0.92	0.66	1.48
PREDICTED: tenascin isoform X4 [Homo sapiens]	1.18	4.77	0.95	0.61	2.01
PREDICTED: spermatid perinuclear RNA-binding protein isoform X3 [Homo sapiens]	0.69	1.25	1.20	1.29	1.48
PREDICTED: actin-related protein 2/3 complex subunit 5-like protein isoform X1 [Homo sapiens]	0.83	0.85	0.53	0.39	0.81
PREDICTED: polypyrimidine tract-binding protein 3 isoform X1 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
PREDICTED: ERV-FRD provirus ancestral Env polyprotein-like isoform X1 [Homo sapiens]	0.50	0.71	0.27	0.11	0.41
PREDICTED: abl interactor 1 isoform X2 [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
PREDICTED: abl interactor 1 isoform X3 [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
PREDICTED: CUGBP Elav-like family member 2 isoform X3 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X4 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X6 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X9 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: phosphoribosyltransferase domain-containing protein 1 isoform X1 [Homo sapiens]	10.14	1.28	1.62	1.42	1.88
PREDICTED: ras suppressor protein 1 isoform X1 [Homo sapiens]	1.76	2.59	1.54	0.98	1.54
PREDICTED: protein FAM107B isoform X3 [Homo sapiens]	0.66	0.99	1.20	1.88	0.97
PREDICTED: adenosine kinase isoform X1 [Homo sapiens]	6.44	1.96	2.00	2.55	1.33
PREDICTED: cytosolic purine 5'-nucleotidase isoform X4 [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
PREDICTED: cytosolic purine 5'-nucleotidase isoform X6 [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
PREDICTED: cytosolic purine 5'-nucleotidase isoform X7 [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
PREDICTED: cytosolic purine 5'-nucleotidase isoform X8 [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
PREDICTED: hexokinase-1 isoform X1 [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
PREDICTED: hexokinase-1 isoform X2 [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
PREDICTED: hexokinase-1 isoform X3 [Homo sapiens]	1.57	1.62	0.90	1.25	0.90
PREDICTED: annexin A7 isoform X1 [Homo sapiens]	5.87	1.44	1.34	1.00	1.25
PREDICTED: annexin A7 isoform X2 [Homo sapiens]	5.87	1.44	1.34	1.00	1.25
PREDICTED: annexin A11 isoform X1 [Homo sapiens]	0.88	1.24	2.16	0.96	1.44
PREDICTED: annexin A11 isoform X2 [Homo sapiens]	0.88	1.24	2.16	0.96	1.44
PREDICTED: pterin-4-alpha-carbinolamine dehydratase isoform X1 [Homo sapiens]	1.71	0.95	0.89	0.83	2.08
PREDICTED: exocyst complex component 6 isoform X1 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X2 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X3 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X4 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X5 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform X3 [Homo sapiens]	0.77	0.82	0.62	0.55	0.68
PREDICTED: serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform X4 [Homo sapiens]	0.77	0.82	0.62	0.55	0.68

sapiens]					
PREDICTED: retinol-binding protein 4 isoform X1 [Homo sapiens]	0.39	0.49	0.17	0.12	0.54
PREDICTED: vinculin isoform X1 [Homo sapiens]	0.88	1.96	1.27	1.29	1.30
PREDICTED: vinculin isoform X2 [Homo sapiens]	0.88	1.96	1.27	1.29	1.30
PREDICTED: xaa-Pro aminopeptidase 1 isoform X1 [Homo sapiens]	1.00	0.91	1.18	1.65	0.93
PREDICTED: xaa-Pro aminopeptidase 1 isoform X2 [Homo sapiens]	1.00	0.91	1.18	1.65	0.93
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X1 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X3 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X4 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X5 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X6 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X7 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X8 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X9 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X11 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: STE20-like serine/threonine-protein kinase isoform X1 [Homo sapiens]	0.66	0.85	1.00	1.30	0.84
PREDICTED: disintegrin and metalloproteinase domain-containing protein 8 isoform X1 [Homo sapiens]	1.37	2.71	2.06	6.93	1.63
PREDICTED: hemopexin isoform X1 [Homo sapiens]	0.45	1.00	0.43	0.24	0.76
PREDICTED: integrin-linked protein kinase isoform X3 [Homo sapiens]	0.64	0.84	0.88	1.29	0.84
PREDICTED: integrin-linked protein kinase isoform X4 [Homo sapiens]	0.64	0.84	0.88	1.29	0.84
PREDICTED: lymphocyte-specific protein 1 isoform X1 [Homo sapiens]	0.28	0.81	0.64	0.91	0.88
PREDICTED: lymphocyte-specific protein 1 isoform X4 [Homo sapiens]	0.26	0.76	0.63	0.94	0.82
PREDICTED: CD44 antigen isoform X1 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X2 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X3 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X4 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X5 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X8 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X9 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X10 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: peroxiredoxin-5, mitochondrial isoform X1 [Homo sapiens]	1.41	0.93	1.90	1.21	1.28
PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	0.28	0.64	0.29	0.19	0.74

isoform X1 [Homo sapiens]					
PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)					
isoform X2 [Homo sapiens]	0.28	0.64	0.29	0.19	0.74
PREDICTED: lysosomal Pro-X carboxypeptidase					
isoform X1 [Homo sapiens]	2.38	1.24	1.29	0.62	2.30
PREDICTED: syntaxin-3 isoform X2 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
PREDICTED: syntaxin-3 isoform X4 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
PREDICTED: syntaxin-3 isoform X5 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
PREDICTED: syntaxin-3 isoform X6 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X1 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X3 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X4 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X5 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X6 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X7 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X1 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X2 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X3 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X4 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X5 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X6 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X7 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X8 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X9 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X10 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X11 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X12 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X13 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X14 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X15 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X16 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X19 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: hypoxia up-regulated protein 1 isoform X5 [Homo sapiens]	0.67	1.63	1.92	1.39	1.94
PREDICTED: probable ATP-dependent RNA helicase DDX6 isoform X2 [Homo sapiens]	0.83	1.47	1.58	2.00	1.33
PREDICTED: thymocyte nuclear protein 1 isoform X1 [Homo sapiens]	0.31	1.30	1.18	2.38	1.40
PREDICTED: thymocyte nuclear protein 1 isoform X2 [Homo sapiens]	0.31	1.30	1.18	2.38	1.40
PREDICTED: porphobilinogen deaminase isoform X3	11.91	0.64	0.55	0.24	0.64

[Homo sapiens]					
PREDICTED: coatomer subunit delta isoform X1 [Homo sapiens]	0.33	1.18	4.43	5.93	1.88
PREDICTED: cell surface glycoprotein MUC18 isoform X1 [Homo sapiens]	0.28	1.18	0.35	0.20	0.53
PREDICTED: cell surface glycoprotein MUC18 isoform X2 [Homo sapiens]	0.28	1.18	0.35	0.20	0.53
PREDICTED: complement C1s subcomponent isoform X1 [Homo sapiens]	0.50	1.53	0.95	0.44	0.67
PREDICTED: gamma-aminobutyric acid receptor-associated protein-like 1 isoform X1 [Homo sapiens]	1.57	1.47	1.54	1.00	1.20
PREDICTED: complement C1r subcomponent-like protein isoform X2 [Homo sapiens]	0.14	0.84	0.37	0.08	0.20
PREDICTED: complement C1r subcomponent-like protein isoform X3 [Homo sapiens]	0.14	0.84	0.37	0.08	0.20
PREDICTED: protein mago nashi homolog 2 isoform X1 [Homo sapiens]	2.34	1.59	2.33	3.87	1.61
PREDICTED: scavenger receptor cysteine-rich type 1 protein M130 isoform X2 [Homo sapiens]	2.34	1.53	1.29	2.17	1.63
PREDICTED: scavenger receptor cysteine-rich type 1 protein M130 isoform X3 [Homo sapiens]	2.34	1.53	1.29	2.17	1.63
PREDICTED: prostaglandin E synthase 3 isoform X1 [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
PREDICTED: eukaryotic translation initiation factor 4B isoform X1 [Homo sapiens]	3.75	1.22	1.18	0.95	1.26
PREDICTED: heterogeneous nuclear ribonucleoprotein A1 isoform X1 [Homo sapiens]	1.31	2.20	1.29	1.34	2.30
PREDICTED: ADP-ribosylation factor 3 isoform X1 [Homo sapiens]	0.50	2.45	0.80	0.71	1.24
PREDICTED: keratin, type II cytoskeletal 3 isoform X1 [Homo sapiens]	0.88	2.08	1.87	0.66	3.64
PREDICTED: leukotriene A-4 hydrolase isoform X1 [Homo sapiens]	0.91	1.00	2.56	0.79	1.61
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X1 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X2 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X4 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X5 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X7 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X8 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X9 [Homo sapiens]	0.45	0.83	0.84	2.25	0.91
PREDICTED: nucleosome assembly protein 1-like 1 isoform X1 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
PREDICTED: bridging integrator 2 isoform X1 [Homo sapiens]	0.80	0.96	0.80	0.63	1.94
PREDICTED: bridging integrator 2 isoform X2 [Homo sapiens]	0.80	0.96	0.80	0.63	1.94
PREDICTED: 5'-AMP-activated protein kinase subunit gamma-1 isoform X1 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
PREDICTED: 5'-AMP-activated protein kinase subunit gamma-1 isoform X2 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
PREDICTED: peripherin isoform X1 [Homo sapiens]	0.75	0.28	0.28	0.52	0.22
PREDICTED: disco-interacting protein 2 homolog B isoform X1 [Homo sapiens]	0.21	1.35	0.66	0.78	1.26
PREDICTED: rho GTPase-activating protein 9 isoform X4 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
PREDICTED: rho GTPase-activating protein 9 isoform X5 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
PREDICTED: rho GTPase-activating protein 9 isoform X7 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38

PREDICTED: SWI/SNF complex subunit SMARCC2 isoform X1 [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
PREDICTED: SWI/SNF complex subunit SMARCC2 isoform X2 [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
PREDICTED: SWI/SNF complex subunit SMARCC2 isoform X3 [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
PREDICTED: SWI/SNF complex subunit SMARCC2 isoform X4 [Homo sapiens]	0.66	0.85	0.95	2.25	0.77
PREDICTED: thymopoietin isoform X1 [Homo sapiens]	0.66	0.81	0.49	0.30	0.66
PREDICTED: thymopoietin isoform X3 [Homo sapiens]	0.66	0.81	0.49	0.30	0.66
PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X1 [Homo sapiens]	4.12	0.94	0.77	0.92	0.82
PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X3 [Homo sapiens]	1.93	0.74	0.66	0.50	0.81
PREDICTED: ARF GTPase-activating protein GIT2 isoform X3 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X6 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: periostin isoform X2 [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
PREDICTED: periostin isoform X3 [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
PREDICTED: heat shock protein 105 kDa isoform X2 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	0.77	0.62	0.42	0.22	0.46
PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	0.69	0.58	0.41	0.19	0.46
PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	0.67	0.58	0.42	0.24	0.46
PREDICTED: S-formylglutathione hydrolase isoform X1 [Homo sapiens]	6.30	0.94	1.19	1.38	1.28
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X1 [Homo sapiens]	0.14	1.88	3.83	7.23	4.01
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X2 [Homo sapiens]	0.14	1.88	3.83	7.23	4.01
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X3 [Homo sapiens]	0.14	1.88	3.83	7.23	4.01
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X4 [Homo sapiens]	0.14	1.88	3.83	7.23	4.01
PREDICTED: high mobility group protein B1 isoform X3 [Homo sapiens]	0.50	1.62	1.60	2.22	1.46
PREDICTED: high mobility group protein B1 isoform X6 [Homo sapiens]	0.50	1.62	1.60	2.22	1.46
PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X2 [Homo sapiens]	1.64	1.57	1.75	1.54	1.45
PREDICTED: proteasome subunit beta type-5 isoform X1 [Homo sapiens]	4.50	1.90	0.76	0.45	2.68
PREDICTED: copine-6 isoform X1 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: copine-6 isoform X2 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: dmX-like protein 2 isoform X1 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
PREDICTED: dmX-like protein 2 isoform X2 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
PREDICTED: dmX-like protein 2 isoform X3 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
PREDICTED: dmX-like protein 2 isoform X4 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
PREDICTED: pro-interleukin-16 isoform X1 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
PREDICTED: pro-interleukin-16 isoform X2 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
PREDICTED: pro-interleukin-16 isoform X3 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
PREDICTED: pro-interleukin-16 isoform X4 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28

PREDICTED: pro-interleukin-16 isoform X5 [Homo sapiens]	0.26	0.71	0.81	1.22	1.28
PREDICTED: protein unc-13 homolog C isoform X1 [Homo sapiens]	0.77	0.96	0.49	0.45	0.92
PREDICTED: protein unc-13 homolog C isoform X2 [Homo sapiens]	0.77	0.96	0.49	0.45	0.92
PREDICTED: pyruvate kinase PKM isoform X1 [Homo sapiens]	0.88	0.95	1.60	1.69	1.27
PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	0.88	0.95	1.60	1.69	1.27
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform X3 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform X4 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform X5 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
PREDICTED: dual specificity mitogen-activated protein kinase kinase 1 isoform X2 [Homo sapiens]	2.19	0.77	2.29	1.34	1.88
PREDICTED: beta-2-microglobulin isoform X1 [Homo sapiens]	0.69	2.05	0.76	0.66	0.89
PREDICTED: ras-related protein Rab-27A isoform X3 [Homo sapiens]	2.38	1.19	1.40	3.26	1.28
PREDICTED: sorting nexin-1 isoform X1 [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
PREDICTED: sorting nexin-1 isoform X2 [Homo sapiens]	1.24	0.88	0.82	1.34	1.61
PREDICTED: tropomyosin alpha-1 chain isoform X11 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X12 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X13 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X14 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X15 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X16 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X17 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: tropomyosin alpha-1 chain isoform X18 [Homo sapiens]	3.90	0.64	1.00	1.28	0.76
PREDICTED: SAFB-like transcription modulator isoform X1 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: talin-2 isoform X8 [Homo sapiens]	2.38	0.82	1.21	1.35	2.39
PREDICTED: tyrosine-protein kinase Fes/Fps isoform X4 [Homo sapiens]	2.33	2.59	0.81	0.51	0.92
PREDICTED: tyrosine-protein kinase Fes/Fps isoform X6 [Homo sapiens]	2.33	2.59	0.81	0.51	0.92
PREDICTED: aminopeptidase N isoform X1 [Homo sapiens]	0.88	1.44	1.87	0.79	1.50
PREDICTED: ras GTPase-activating-like protein IQGAP1 isoform X1 [Homo sapiens]	2.38	0.97	1.18	1.28	1.74
PREDICTED: hemoglobin subunit zeta isoform X1 [Homo sapiens]	126.77	2.45	1.54	0.32	0.96
PREDICTED: putative RNA-binding protein Luc7-like 1 isoform X2 [Homo sapiens]	0.39	0.77	0.58	0.32	0.51
PREDICTED: putative RNA-binding protein Luc7-like 1 isoform X3 [Homo sapiens]	0.39	0.77	0.58	0.32	0.51
PREDICTED: eukaryotic translation initiation factor 5A-1 isoform X5 [Homo sapiens]	10.46	0.78	1.43	1.86	1.30
PREDICTED: rap1 GTPase-activating protein 2 isoform X1 [Homo sapiens]	0.91	0.84	0.58	0.39	0.54
PREDICTED: rap1 GTPase-activating protein 2 isoform X2 [Homo sapiens]	0.91	0.84	0.58	0.39	0.54
PREDICTED: rap1 GTPase-activating protein 2 isoform	0.91	0.84	0.58	0.39	0.54

X3 [Homo sapiens]					
PREDICTED: protein flightless-1 homolog isoform X1 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
PREDICTED: protein flightless-1 homolog isoform X2 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
PREDICTED: protein flightless-1 homolog isoform X4 [Homo sapiens]	2.00	1.40	0.79	2.48	0.94
PREDICTED: E3 ubiquitin-protein ligase RNF167 isoform X3 [Homo sapiens]		0.91	2.21	2.35	1.48
PREDICTED: E3 ubiquitin-protein ligase RNF167 isoform X5 [Homo sapiens]		0.91	2.21	2.35	1.48
PREDICTED: E3 ubiquitin-protein ligase RNF167 isoform X7 [Homo sapiens]		0.91	2.21	2.35	1.48
PREDICTED: myosin-10 isoform X1 [Homo sapiens]	0.95	0.94	1.43	1.74	2.45
PREDICTED: myosin-10 isoform X2 [Homo sapiens]	0.95	0.94	1.43	1.74	2.45
PREDICTED: myosin-10 isoform X3 [Homo sapiens]	0.95	0.94	1.43	1.74	2.45
PREDICTED: ankyrin repeat and FYVE domain-containing protein 1 isoform X1 [Homo sapiens]	1.31	1.51	1.72	1.21	1.28
PREDICTED: alpha-2-antiplasmin isoform X1 [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
PREDICTED: alpha-2-antiplasmin isoform X2 [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
PREDICTED: alpha-2-antiplasmin isoform X3 [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
PREDICTED: alpha-2-antiplasmin isoform X6 [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
PREDICTED: dual specificity mitogen-activated protein kinase kinase 3 isoform X2 [Homo sapiens]	0.95	0.77	0.68	0.52	0.81
PREDICTED: arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 isoform X1 [Homo sapiens]	5.93	2.71	0.82	0.67	1.23
PREDICTED: AP-2 complex subunit beta isoform X2 [Homo sapiens]	1.89	1.19	0.83	1.77	0.83
PREDICTED: fructose-bisphosphate aldolase C isoform X1 [Homo sapiens]	1.82	1.62	0.92	0.85	0.89
PREDICTED: fructose-bisphosphate aldolase C isoform X3 [Homo sapiens]	1.82	1.62	0.92	0.85	0.89
PREDICTED: flotillin-2 isoform X1 [Homo sapiens]	0.23	0.93	0.31	0.26	0.44
PREDICTED: flotillin-2 isoform X3 [Homo sapiens]	0.23	0.93	0.31	0.26	0.44
PREDICTED: flotillin-2 isoform X4 [Homo sapiens]	0.23	0.93	0.31	0.26	0.44
PREDICTED: coronin-6 isoform X2 [Homo sapiens]	0.35	0.91	1.24	1.80	1.28
PREDICTED: coronin-6 isoform X3 [Homo sapiens]	0.35	0.91	1.24	1.80	1.28
PREDICTED: coronin-6 isoform X5 [Homo sapiens]	0.35	0.91	1.24	1.80	1.28
PREDICTED: coronin-6 isoform X8 [Homo sapiens]	0.35	0.91	1.24	1.80	1.28
PREDICTED: coronin-6 isoform X11 [Homo sapiens]	0.35	0.91	1.24	1.80	1.28
PREDICTED: septin-9 isoform X5 [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
PREDICTED: clathrin heavy chain 1 isoform X2 [Homo sapiens]	1.76	0.85	0.90	2.01	0.78
PREDICTED: polymerase I and transcript release factor isoform X2 [Homo sapiens]	0.46	0.16	0.12	0.07	0.25
PREDICTED: interferon-induced 35 kDa protein isoform X1 [Homo sapiens]	0.64	0.97	2.76	1.35	1.48
PREDICTED: keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]	2.38	0.78	0.45	0.18	0.56
PREDICTED: keratin, type I cytoskeletal 17 isoform X1 [Homo sapiens]	0.83	0.88	0.94	0.62	0.93
PREDICTED: ATP-citrate synthase isoform X1 [Homo sapiens]	3.21	0.96	1.37	1.42	0.94
PREDICTED: ATP-citrate synthase isoform X2 [Homo sapiens]	3.21	0.96	1.37	1.42	0.94
PREDICTED: ATP-citrate synthase isoform X3 [Homo sapiens]	3.21	0.96	1.37	1.42	0.94

PREDICTED: dual specificity mitogen-activated protein kinase kinase 6 isoform X2 [Homo sapiens]	0.77	0.63	0.71	0.55	0.74
PREDICTED: band 3 anion transport protein isoform X1 [Homo sapiens]	4.99	2.71	0.82	0.44	0.82
PREDICTED: band 3 anion transport protein isoform X2 [Homo sapiens]	4.99	2.71	0.82	0.44	0.82
PREDICTED: signal transducer and activator of transcription 3 isoform X4 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
PREDICTED: signal transducer and activator of transcription 3 isoform X5 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
PREDICTED: signal transducer and activator of transcription 3 isoform X6 [Homo sapiens]	2.00	0.70	1.19	2.80	0.89
PREDICTED: signal transducer and activator of transcription 5A isoform X4 [Homo sapiens]	0.45	0.68	1.19	1.98	0.76
PREDICTED: signal transducer and activator of transcription 5B isoform X1 [Homo sapiens]	0.45	0.68	1.19	1.98	0.76
PREDICTED: signal transducer and activator of transcription 5B isoform X2 [Homo sapiens]	0.39	0.76	0.77	2.38	0.58
PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate isoform X1 [Homo sapiens]	10.46	0.82	0.46	0.42	0.53
PREDICTED: THO complex subunit 4 isoform X1 [Homo sapiens]	0.77	1.26	1.28	2.09	1.36
PREDICTED: coiled-coil domain-containing protein 57 isoform X3 [Homo sapiens]	2.58	0.70	2.07	2.51	2.60
PREDICTED: proteasome subunit alpha type-7-like isoform X1 [Homo sapiens]	5.20	1.41	2.10	1.65	1.58
PREDICTED: mitogen-activated protein kinase 4 isoform X2 [Homo sapiens]	2.11	1.96	2.07	2.33	2.05
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X2 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X4 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X7 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: asparagine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	8.60	1.00	2.79	5.14	1.40
PREDICTED: calponin-1 isoform X1 [Homo sapiens]	0.91	0.79	0.95	1.66	1.47
PREDICTED: neurocan core protein isoform X2 [Homo sapiens]	0.80	2.59	0.95	0.58	1.23
PREDICTED: 6-phosphogluconolactonase isoform X1 [Homo sapiens]	0.57	0.94	0.90	0.83	2.60
PREDICTED: interleukin enhancer-binding factor 3 isoform X2 [Homo sapiens]	1.31	1.25	2.20	4.02	2.13
PREDICTED: leukotriene-B(4) omega-hydroxylase 2 isoform X2 [Homo sapiens]	0.69	2.32	0.88	0.51	1.37
PREDICTED: lysosomal alpha-mannosidase isoform X1 [Homo sapiens]	3.61	1.79	1.26	0.66	1.35
PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha isoform X1 [Homo sapiens]	0.91	0.69	0.78	1.00	0.80
PREDICTED: tropomyosin alpha-4 chain isoform X1 [Homo sapiens]	2.58	0.95	1.24	0.80	0.96
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X1 [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X2 [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X4 [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
PREDICTED: carcinoembryonic antigen-related cell adhesion molecule 8 isoform X1 [Homo sapiens]	2.11	1.26	0.67	0.42	0.82
PREDICTED: carcinoembryonic antigen-related cell adhesion molecule 8 isoform X2 [Homo sapiens]	2.11	2.08	0.64	0.41	0.81
PREDICTED: kallikrein-11 isoform X1 [Homo sapiens]	2.15	0.54	0.23	0.15	0.41
PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform X1 [Homo sapiens]	1.21	1.45	1.70	1.59	1.26
PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform X3 [Homo sapiens]	1.21	1.45	1.70	1.59	1.26

PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform X4 [Homo sapiens]	1.21	1.45	1.70	1.59	1.26
PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform X6 [Homo sapiens]	1.21	1.45	1.70	1.59	1.26
PREDICTED: delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial isoform X1 [Homo sapiens]	0.57	1.28	2.05	1.26	1.25
PREDICTED: TFIIH basal transcription factor complex helicase XPD subunit isoform X1 [Homo sapiens]	0.28	1.39	3.23	4.06	2.56
PREDICTED: rRNA 2'-O-methyltransferase fibrillarin isoform X1 [Homo sapiens]	0.77	0.85	0.31	0.15	0.50
PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 1 isoform X1 [Homo sapiens]	2.19	2.25	2.06	2.17	1.50
PREDICTED: persulfide dioxygenase ETHE1, mitochondrial isoform X2 [Homo sapiens]	2.00	1.51	0.74	0.55	0.79
PREDICTED: persulfide dioxygenase ETHE1, mitochondrial isoform X3 [Homo sapiens]	2.00	1.51	0.74	0.55	0.79
PREDICTED: glucose-6-phosphate isomerase isoform X2 [Homo sapiens]	0.88	1.27	1.47	1.45	1.44
PREDICTED: apolipoprotein E isoform X1 [Homo sapiens]	0.41	0.85	0.44	0.29	0.39
PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa isoform X2 [Homo sapiens]	0.28	2.20	1.64	1.57	1.45
PREDICTED: vasodilator-stimulated phosphoprotein isoform X1 [Homo sapiens]	0.25	0.87	2.16	3.76	1.47
PREDICTED: vasodilator-stimulated phosphoprotein isoform X2 [Homo sapiens]	0.50	0.91	1.46	1.82	1.94
PREDICTED: alpha-actinin-4 isoform X1 [Homo sapiens]	0.75	2.08	1.51	1.71	1.18
PREDICTED: alpha-actinin-4 isoform X2 [Homo sapiens]	0.75	2.08	1.51	1.71	1.18
PREDICTED: calpain small subunit 1 isoform X1 [Homo sapiens]	2.02	0.91	0.89	0.62	0.98
PREDICTED: calpain small subunit 1 isoform X3 [Homo sapiens]	0.88	0.95	2.68	0.73	2.16
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X1 [Homo sapiens]	0.39	0.96	0.89	1.30	0.93
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X2 [Homo sapiens]	0.39	0.96	0.89	1.30	0.93
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X3 [Homo sapiens]	0.39	0.96	0.89	1.30	0.93
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X4 [Homo sapiens]	0.77	2.08	0.93	0.92	0.91
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X5 [Homo sapiens]	1.34	0.85	0.64	0.92	0.76
PREDICTED: programmed cell death protein 5 isoform X1 [Homo sapiens]	2.02	0.96	0.94	0.95	0.94
PREDICTED: glia maturation factor gamma isoform X1 [Homo sapiens]	0.64	0.89	1.63	3.12	1.78
PREDICTED: adenosine deaminase isoform X1 [Homo sapiens]	1.79	2.45	1.36	1.73	1.36
PREDICTED: adenosylhomocysteinase isoform X2 [Homo sapiens]	4.38	0.95	1.50	1.56	2.45
PREDICTED: RNA-binding protein Raly isoform X3 [Homo sapiens]	0.54	0.94	0.98	0.98	0.90
PREDICTED: deoxynucleoside triphosphate triphosphohydrolase SAMHD1 isoform X1 [Homo sapiens]	2.79	0.93	1.46	2.05	0.97
PREDICTED: glutathione synthetase isoform X2 [Homo sapiens]	4.78	1.44	2.10	1.78	1.79
PREDICTED: phospholipid transfer protein isoform X1 [Homo sapiens]	1.61	1.97	0.66	0.46	0.80
PREDICTED: phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein isoform X1 [Homo sapiens]		0.68	0.80	1.91	0.68
PREDICTED: engulfment and cell motility protein 2 isoform X5 [Homo sapiens]	0.14	0.57	1.21	1.70	0.74
PREDICTED: engulfment and cell motility protein 2 isoform X8 [Homo sapiens]	0.14	0.57	1.21	1.70	0.74

PREDICTED: bactericidal permeability-increasing protein isoform X1 [Homo sapiens]	0.83	1.74	1.24	1.88	1.62
PREDICTED: bactericidal permeability-increasing protein isoform X2 [Homo sapiens]	0.80	1.40	1.43	1.47	1.34
PREDICTED: serine/threonine-protein kinase 4 isoform X1 [Homo sapiens]	0.75	0.66	0.56	0.74	0.67
PREDICTED: serine/threonine-protein kinase 4 isoform X2 [Homo sapiens]	0.75	0.66	0.56	0.74	0.67
PREDICTED: serine/threonine-protein kinase 4 isoform X4 [Homo sapiens]	0.75	0.66	0.56	0.74	0.67
PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isoform X1 [Homo sapiens]	15.50	0.85	0.82	0.54	0.99
PREDICTED: 6-phosphofructokinase, liver type isoform X2 [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
PREDICTED: 6-phosphofructokinase, liver type isoform X3 [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
PREDICTED: 6-phosphofructokinase, liver type isoform X4 [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
PREDICTED: pyridoxal kinase isoform X1 [Homo sapiens]	1.00	0.94	0.89	0.62	0.99
PREDICTED: pyridoxal kinase isoform X2 [Homo sapiens]	1.00	0.94	0.89	0.62	0.99
PREDICTED: pyridoxal kinase isoform X4 [Homo sapiens]	1.00	0.94	0.89	0.62	0.99
PREDICTED: pyridoxal kinase isoform X5 [Homo sapiens]	1.31	0.97	0.98	0.95	1.74
PREDICTED: D-dopachrome decarboxylase-like protein isoform X1 [Homo sapiens]	3.26	0.93	0.83	0.85	0.92
PREDICTED: nuclear pore complex protein Nup50 isoform X3 [Homo sapiens]	0.39	0.94	1.00	1.42	0.96
PREDICTED: protein kinase C and casein kinase substrate in neurons protein 2 isoform X1 [Homo sapiens]	1.00	0.79	0.88	1.27	0.96
PREDICTED: RNA-binding protein EWS isoform X1 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
PREDICTED: RNA-binding protein EWS isoform X2 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
PREDICTED: heparin cofactor 2 isoform X1 [Homo sapiens]	0.45	0.64	0.45	0.32	0.85
PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X1 [Homo sapiens]	9.20	0.73	0.64	0.66	0.74
PREDICTED: neurofilament heavy polypeptide isoform X1 [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
PREDICTED: apolipoprotein L1 isoform X1 [Homo sapiens]	0.56	0.67	0.37	0.22	0.41
PREDICTED: peroxiredoxin-4 isoform X1 [Homo sapiens]	19.15	0.83	1.43	0.94	1.42
PREDICTED: SH3 domain-containing kinase-binding protein 1 isoform X2 [Homo sapiens]	2.00	1.25	1.48	2.06	1.28
PREDICTED: SH3 domain-containing kinase-binding protein 1 isoform X3 [Homo sapiens]	2.00	1.25	1.48	2.06	1.28
PREDICTED: SH3 domain-containing kinase-binding protein 1 isoform X4 [Homo sapiens]	2.00	1.25	1.48	2.06	1.28
PREDICTED: cAMP-dependent protein kinase catalytic subunit PRKX isoform X2 [Homo sapiens]	0.64	2.08	1.27	1.77	1.19
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X1 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X4 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X5 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
PREDICTED: spermine synthase isoform X1 [Homo sapiens]	2.00	0.98	0.75	0.63	0.85
PREDICTED: spermine synthase isoform X2 [Homo sapiens]	2.00	0.98	0.75	0.63	0.85
PREDICTED: ubiquitin-like modifier-activating enzyme 1 isoform X1 [Homo sapiens]	2.02	0.98	0.97	0.92	0.94

PREDICTED: ubiquitin-like modifier-activating enzyme 1 isoform X2 [Homo sapiens]	2.02	0.98	0.97	0.92	0.94
PREDICTED: probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform X1 [Homo sapiens]	1.54	0.91	0.58	0.67	0.77
PREDICTED: probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform X2 [Homo sapiens]	1.54	0.91	0.58	0.67	0.77
PREDICTED: moesin isoform X1 [Homo sapiens]	0.64	2.20	1.24	1.51	1.25
PREDICTED: protein PBDC1 isoform X1 [Homo sapiens]	1.71	0.84	0.58	0.41	0.63
PREDICTED: collagen alpha-5(IV) chain isoform X1 [Homo sapiens]	1.28	0.76	0.56	0.69	0.76
PREDICTED: serine/threonine-protein kinase PAK 3 isoform X3 [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
PREDICTED: thyroxine-binding globulin isoform X1 [Homo sapiens]	0.46	1.51	0.45	0.28	0.70
PREDICTED: dedicator of cytokinesis protein 11 isoform X1 [Homo sapiens]	8.36	1.25	0.61	0.49	0.75
PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]	8.36	1.25	0.61	0.49	0.75
PREDICTED: coagulation factor IX isoform X2 [Homo sapiens]	0.35	0.50	0.29	0.14	0.31
PREDICTED: septin-6 isoform X1 [Homo sapiens]	1.44	0.94	1.39	1.54	1.74
PREDICTED: HIV Tat-specific factor 1 isoform X1 [Homo sapiens]	0.67	0.62	0.22	0.11	0.35
PREDICTED: cullin-4B isoform X1 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
PREDICTED: rho guanine nucleotide exchange factor 6 isoform X3 [Homo sapiens]	1.21	0.87	0.55	0.77	0.87
PREDICTED: rho guanine nucleotide exchange factor 6 isoform X5 [Homo sapiens]	2.11	0.99	0.78	0.68	1.48
PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X1 [Homo sapiens]	0.88	1.19	1.46	2.16	1.24
PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X2 [Homo sapiens]	0.88	1.19	1.46	2.16	1.24
PREDICTED: high mobility group protein B3 isoform X1 [Homo sapiens]	0.64	0.76	0.53	0.69	0.78
PREDICTED: high mobility group protein B3 isoform X2 [Homo sapiens]	0.64	0.76	0.53	0.69	0.78
PREDICTED: high mobility group protein B3 isoform X3 [Homo sapiens]	0.64	0.76	0.53	0.69	0.78
PREDICTED: methyl-CpG-binding protein 2 isoform X1 [Homo sapiens]		0.42	1.87	1.00	1.65
PREDICTED: ATP-dependent RNA helicase DDX3Y isoform X1 [Homo sapiens]	0.75	0.93	0.99	1.71	2.76
PREDICTED: importin-5 isoform X5 [Homo sapiens]	2.19	0.94	0.70	1.89	0.64
PREDICTED: tripeptidyl-peptidase 2 isoform X1 [Homo sapiens]	4.31	2.71	1.34	1.39	1.23
PREDICTED: tripeptidyl-peptidase 2 isoform X2 [Homo sapiens]	4.31	2.71	1.34	1.39	1.23
PREDICTED: tripeptidyl-peptidase 2 isoform X3 [Homo sapiens]	4.31	2.71	1.34	1.39	1.23
PREDICTED: tripeptidyl-peptidase 2 isoform X4 [Homo sapiens]	4.31	2.71	1.34	1.39	1.23
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X2 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X3 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X4 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X5 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X6 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X7 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7	1.21	0.87	0.49	0.26	0.87

isoform X8 [Homo sapiens]					
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X11 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: nuclear transport factor 2 isoform X1 [Homo sapiens]	29.69	1.26	2.28	2.52	2.02
PREDICTED: haptoglobin isoform X1 [Homo sapiens]	0.62	5.10	3.10	1.74	4.51
PREDICTED: vacuolar protein sorting-associated protein 35 isoform X2 [Homo sapiens]	1.31	0.85	0.56	0.57	0.68
PREDICTED: U6 snRNA phosphodiesterase isoform X1 [Homo sapiens]	4.07	0.73	0.50	0.33	0.50
PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X2 [Homo sapiens]	1.57	1.45	1.37	2.24	1.58
PREDICTED: NEDD8-activating enzyme E1 regulatory subunit isoform X2 [Homo sapiens]	2.34	1.22	1.37	1.64	1.20
PREDICTED: N-acetylgalactosamine-6-sulfatase isoform X1 [Homo sapiens]	0.54	1.40	0.90	0.77	1.61
PREDICTED: N-acetylgalactosamine-6-sulfatase isoform X2 [Homo sapiens]	0.54	1.40	0.90	0.77	1.61
PREDICTED: myosin regulatory light chain 12A isoform X2 [Homo sapiens]	0.91	0.87	1.60	1.19	0.98
PREDICTED: structural maintenance of chromosomes flexible hinge domain-containing protein 1 isoform X1 [Homo sapiens]	5.87	0.78	1.00	1.97	0.75
PREDICTED: neutrophil elastase isoform X1 [Homo sapiens]	0.77	1.76	2.56	0.57	0.98
PREDICTED: polypyrimidine tract-binding protein 1 isoform X1 [Homo sapiens]	1.57	1.51	1.58	1.91	1.45
PREDICTED: polypyrimidine tract-binding protein 1 isoform X2 [Homo sapiens]	1.57	1.51	1.58	1.91	1.45
PREDICTED: proto-oncogene vav isoform X1 [Homo sapiens]	0.75	0.88	0.56	0.52	0.78
PREDICTED: signal-regulatory protein beta-1 isoform X2 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: signal-regulatory protein beta-1 isoform X4 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: signal-regulatory protein beta-1 isoform X5 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: tyrosine-protein phosphatase non-receptor type substrate 1 isoform X1 [Homo sapiens]	0.50	1.56	1.21	0.94	1.52
PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]	2.17	0.93	0.99	0.75	0.81
PREDICTED: ral GTPase-activating protein subunit alpha-2 isoform X1 [Homo sapiens]	149.10	0.78	1.21	0.31	1.24
PREDICTED: attractin isoform X1 [Homo sapiens]	0.39	0.92	0.40	0.24	0.54
PREDICTED: attractin isoform X2 [Homo sapiens]	0.41	0.93	0.44	0.26	0.55
PREDICTED: clathrin heavy chain 2 isoform X4 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: ras-related GTP-binding protein B isoform X1 [Homo sapiens]	0.77	0.89	0.40	0.27	0.58
PREDICTED: ras-related GTP-binding protein B isoform X2 [Homo sapiens]	0.77	0.89	0.40	0.27	0.58
PREDICTED: ras-related GTP-binding protein B isoform X3 [Homo sapiens]	0.77	0.89	0.40	0.27	0.58
PREDICTED: ficolin-1 isoform X1 [Homo sapiens]	0.31	2.08	0.66	0.56	0.76
PREDICTED: dipeptidyl peptidase 2 isoform X1 [Homo sapiens]	0.91	1.59	0.98	0.65	1.23
PREDICTED: coagulation factor X isoform X1 [Homo sapiens]	0.21	0.69	0.27	0.15	0.46
PREDICTED: nuclear pore complex protein Nup214 isoform X1 [Homo sapiens]	0.43	2.45	1.57	2.59	1.37
PREDICTED: nuclear pore complex protein Nup214 isoform X2 [Homo sapiens]	0.43	2.45	1.57	2.59	1.37
PREDICTED: nuclear pore complex protein Nup214 isoform X3 [Homo sapiens]	0.43	2.45	1.57	2.59	1.37
PREDICTED: nuclear pore complex protein Nup214	0.43	2.45	1.57	2.59	1.37

isoform X4 [Homo sapiens]					
PREDICTED: unconventional myosin-I α isoform X1 [Homo sapiens]	0.80	0.89	1.50	2.47	2.08
PREDICTED: unconventional myosin-I α isoform X2 [Homo sapiens]	0.80	0.89	1.50	2.47	2.08
PREDICTED: unconventional myosin-I α isoform X3 [Homo sapiens]	0.80	0.88	1.77	3.12	2.37
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X1 [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X2 [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X3 [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X4 [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X6 [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
PREDICTED: PML-RARA-regulated adapter molecule 1 isoform X1 [Homo sapiens]	0.33	0.82	1.52	2.49	1.74
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	0.77	1.73	1.38	1.43	1.26
PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	0.77	1.73	1.38	1.43	1.26
PREDICTED: valine--tRNA ligase isoform X1 [Homo sapiens]	0.77	0.68	0.58	0.44	0.69
PREDICTED: allograft inflammatory factor 1 isoform X1 [Homo sapiens]	0.77	0.98	1.31	1.23	2.39
PREDICTED: allograft inflammatory factor 1 isoform X3 [Homo sapiens]	0.77	0.98	1.31	1.23	2.39
PREDICTED: allograft inflammatory factor 1 isoform X2 [Homo sapiens]	0.77	0.98	1.31	1.23	2.39
PREDICTED: N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 isoform X1 [Homo sapiens]	0.57	0.80	0.50	0.49	0.57
PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo sapiens]	0.88	0.91	0.76	0.73	0.75
PREDICTED: valine--tRNA ligase isoform X1 [Homo sapiens]	0.77	0.68	0.58	0.44	0.69
PREDICTED: HLA class I histocompatibility antigen, A-2 alpha chain isoform X3 [Homo sapiens]	0.83	0.96	0.67	0.34	0.80
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	0.77	1.73	1.38	1.43	1.26
PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	0.77	1.73	1.38	1.43	1.26
PREDICTED: puromycin-sensitive aminopeptidase-like protein-like isoform X1 [Homo sapiens]	1.31	0.84	1.00	1.63	0.90
PREDICTED: trypsin-2 isoform X1 [Homo sapiens]	1.61	0.48	0.20	0.13	0.32
PREDICTED: general transcription factor II-I repeat domain-containing protein 2A isoform X1 [Homo sapiens]	0.31	0.45	0.31	0.12	0.29
PREDICTED: clathrin heavy chain 2 isoform X1 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: clathrin heavy chain 2 isoform X2 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	1.31	1.90	2.68	2.33	1.63
PREDICTED: myosin regulatory light chain 12B-like [Homo sapiens]	0.83	0.87	0.89	0.88	0.95
PREDICTED: small ubiquitin-related modifier 2-like [Homo sapiens]	1.64	0.99	1.22	1.47	0.99
PREDICTED: ERV-FRD provirus ancestral Env polyprotein-like isoform X1 [Homo sapiens]	0.50	0.71	0.27	0.11	0.41
PREDICTED: prothymosin alpha-like [Homo sapiens]	0.62	0.94	2.09	2.83	0.81
PREDICTED: sulfotransferase 1A3/1A4-like isoform X1 [Homo sapiens]	0.45	0.83	0.68	0.85	2.53
PREDICTED: puromycin-sensitive aminopeptidase-like protein-like isoform X2 [Homo sapiens]	0.66	0.80	0.88	1.59	0.82

F-actin-capping protein subunit beta isoform 4 [Homo sapiens]	0.62	1.30	1.30	1.56	1.74
eukaryotic peptide chain release factor subunit 1 isoform 3 [Homo sapiens]	1.93	1.30	1.64	1.82	1.27
adenosine deaminase CECR1 isoform a precursor [Homo sapiens]	1.24	1.27	1.44	1.24	2.01
adenosine deaminase CECR1 isoform c [Homo sapiens]	1.24	1.27	1.44	1.24	2.01
adenosine deaminase CECR1 isoform d [Homo sapiens]	1.24	1.27	1.44	1.24	2.01
proteasome subunit alpha type-6 isoform b [Homo sapiens]	1.57	0.91	1.28	0.88	0.96
proteasome subunit alpha type-6 isoform c [Homo sapiens]	1.57	0.99	1.28	0.88	0.96
matrin-3 isoform c [Homo sapiens]	0.77	2.01	17.85	4.09	4.67
serine/threonine-protein kinase 25 isoform 4 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
serine/threonine-protein kinase 25 isoform 3 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
minor histocompatibility protein HA-1 isoform 3 [Homo sapiens]	0.45	0.68	0.50	0.79	0.75
minor histocompatibility protein HA-1 isoform 4 [Homo sapiens]	0.45	0.68	0.50	0.79	0.75
plastin-3 isoform 3 [Homo sapiens]	0.69	1.22	1.76	1.81	1.46
plastin-3 isoform 4 [Homo sapiens]	0.69	1.22	1.76	1.81	1.46
osteoclast-associated immunoglobulin-like receptor isoform 1 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
osteoclast-associated immunoglobulin-like receptor isoform 3 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
osteoclast-associated immunoglobulin-like receptor isoform 4 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
osteoclast-associated immunoglobulin-like receptor isoform 5 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
osteoclast-associated immunoglobulin-like receptor isoform 6 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
osteoclast-associated immunoglobulin-like receptor isoform 7 precursor [Homo sapiens]	1.82	0.84	0.49	0.27	0.56
isocitrate dehydrogenase [NADP] cytoplasmic [Homo sapiens]	2.00	1.39	2.09	2.30	1.83
malate dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]	7.48	1.28	2.00	1.35	1.61
malate dehydrogenase, mitochondrial isoform 3 [Homo sapiens]	2.19	2.59	1.80	1.46	1.41
protein phosphatase 1 regulatory subunit 7 isoform 6 [Homo sapiens]	1.61	1.19	2.29	1.44	1.23
protein phosphatase 1 regulatory subunit 7 isoform 7 [Homo sapiens]	1.61	1.21	2.29	1.44	1.23
EH domain-containing protein 1 isoform 1 [Homo sapiens]	3.21	0.85	0.77	0.75	0.96
EH domain-containing protein 1 isoform 2 [Homo sapiens]	3.21	0.85	0.77	0.75	0.96
sorting nexin-5 isoform b [Homo sapiens]	0.33	0.77	0.96	1.28	2.30
complement C2 isoform 4 [Homo sapiens]	0.41	1.96	0.58	0.32	0.67
complement C2 isoform 5 [Homo sapiens]	0.39	1.96	0.71	0.32	0.67
complement C2 isoform 6 precursor [Homo sapiens]	0.25	1.27	0.71	0.26	0.58
protein phosphatase 1 regulatory subunit 7 isoform 2 [Homo sapiens]	1.61	1.19	2.29	1.44	1.23
protein phosphatase 1 regulatory subunit 7 isoform 3 [Homo sapiens]	1.61	1.21	2.29	1.44	1.23
protein phosphatase 1 regulatory subunit 7 isoform 4 [Homo sapiens]	1.61	1.21	2.29	1.44	1.23
protein phosphatase 1 regulatory subunit 7 isoform 5 [Homo sapiens]	1.61	1.19	2.29	1.44	1.23
nucleolar protein of 40 kDa isoform g [Homo sapiens]	30.15	2.08	0.64	0.22	0.87

nucleolar protein of 40 kDa isoform h [Homo sapiens]	30.15	2.08	0.64	0.22	0.87
guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform 2 [Homo sapiens]	0.64	1.22	1.26	0.79	0.89
guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform 1 [Homo sapiens]	0.64	1.22	1.26	0.79	0.89
prostaglandin E synthase 3 isoform c [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
prostaglandin E synthase 3 isoform e [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
prostaglandin E synthase 3 isoform d [Homo sapiens]	1.82	1.96	0.94	0.97	1.42
prostaglandin E synthase 3 isoform b [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
prostaglandin E synthase 3 isoform f [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
ubiquitin-conjugating enzyme E2 variant 1 isoform g [Homo sapiens]	8.90	1.26	1.36	1.27	1.29
ubiquitin-conjugating enzyme E2 variant 1 isoform h [Homo sapiens]	13.07	1.31	2.09	1.94	1.68
ubiquitin-conjugating enzyme E2 variant 1 isoform i [Homo sapiens]	15.20	1.55	2.00	1.93	1.74
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 3 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 4 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 5 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 6 [Homo sapiens]	1.64	1.27	2.01	1.99	1.37
noelin isoform 5 [Homo sapiens]	0.31	0.91	0.39	0.20	0.56
noelin isoform 4 precursor [Homo sapiens]	0.31	0.91	0.39	0.20	0.56
stress-induced-phosphoprotein 1 isoform a [Homo sapiens]	4.26	0.95	1.46	2.05	1.47
stress-induced-phosphoprotein 1 isoform c [Homo sapiens]	3.52	0.94	1.44	2.06	1.47
lamin isoform E [Homo sapiens]	0.31	0.08	0.14	0.05	0.13
lamin isoform C [Homo sapiens]	0.16	0.08	0.14	0.05	0.13
lamin isoform A-delta50 [Homo sapiens]	0.16	0.08	0.14	0.05	0.13
acyl-CoA-binding protein isoform 1 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
acyl-CoA-binding protein isoform 7 [Homo sapiens]	2.00	1.25	2.13	2.57	1.88
protein disulfide-isomerase A6 isoform a [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
protein disulfide-isomerase A6 isoform c [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
protein disulfide-isomerase A6 isoform e precursor [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
protein disulfide-isomerase A6 isoform b [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
leucine-rich repeat flightless-interacting protein 2 isoform 4 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
phosphoribosyltransferase domain-containing protein 1 isoform 2 [Homo sapiens]	10.14	1.28	1.62	1.42	1.88
T-complex protein 1 subunit theta isoform 2 [Homo sapiens]	3.47	1.26	0.98	1.34	1.35
T-complex protein 1 subunit theta isoform 4 [Homo sapiens]	3.47	1.26	0.98	1.34	1.35
T-complex protein 1 subunit theta isoform 3 [Homo sapiens]	3.47	1.26	0.98	1.34	1.35
COP9 signalosome complex subunit 7b isoform a [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
COP9 signalosome complex subunit 7b isoform d [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
COP9 signalosome complex subunit 7b isoform c [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
septin-2 isoform b [Homo sapiens]	3.39	1.51	2.69	0.59	0.87
septin-2 isoform c [Homo sapiens]	3.39	1.51	2.69	0.59	0.87

COP9 signalosome complex subunit 7b isoform e [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
beta-soluble NSF attachment protein isoform d [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
stathmin-4 isoform 3 [Homo sapiens]	0.77	0.94	3.60	7.80	1.58
beta-soluble NSF attachment protein isoform c [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
stathmin-4 isoform 4 [Homo sapiens]	0.77	0.94	3.60	7.80	1.58
beta-soluble NSF attachment protein isoform a [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
stathmin-4 isoform 2 [Homo sapiens]	0.77	0.94	3.60	7.80	1.58
E3 ubiquitin-protein ligase TRIP12 isoform a [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
calpastatin isoform n [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
calpastatin isoform o [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
beta-glucuronidase isoform 2 precursor [Homo sapiens]	0.83	1.83	1.80	1.51	1.30
drebrin-like protein isoform d [Homo sapiens]	0.77	0.69	0.80	0.93	0.91
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform 4 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform 2 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
drebrin-like protein isoform e [Homo sapiens]	0.95	0.79	0.68	0.55	0.80
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform 3 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
phosphatidylinositol transfer protein beta isoform isoform 2 [Homo sapiens]	1.31	1.51	0.99	0.75	0.89
phosphatidylinositol transfer protein beta isoform isoform 3 [Homo sapiens]	1.31	1.51	0.99	0.75	0.89
E3 ubiquitin-protein ligase NEDD4 isoform 3 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4 isoform 4 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
E3 ubiquitin-protein ligase NEDD4 isoform 5 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
eukaryotic translation initiation factor 3 subunit J isoform 2 [Homo sapiens]	4.19	0.88	0.93	2.51	2.45
eukaryotic translation initiation factor 3 subunit J isoform 3 [Homo sapiens]	4.19	0.88	0.93	2.51	2.45
ras GTPase-activating-like protein IQGAP2 isoform 2 [Homo sapiens]	1.18	1.30	1.54	1.57	0.96
ras GTPase-activating-like protein IQGAP2 isoform 3 [Homo sapiens]	1.18	0.84	1.54	1.57	0.96
ras GTPase-activating-like protein IQGAP2 isoform 4 [Homo sapiens]	1.18	0.84	1.54	1.57	0.96
calponin-3 isoform 2 [Homo sapiens]	0.91	0.79	0.95	1.66	1.47
cholesteryl ester transfer protein isoform 2 precursor [Homo sapiens]	0.25	0.53	0.40	0.23	0.77
medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform c [Homo sapiens]	1.21	1.26	0.98	0.66	0.83
medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform d precursor [Homo sapiens]	1.21	1.26	0.98	0.66	0.83
medium-chain specific acyl-CoA dehydrogenase, mitochondrial isoform e [Homo sapiens]	1.21	1.26	0.98	0.66	0.83
3'(2'),5'-bisphosphate nucleotidase 1 isoform 3 [Homo sapiens]	2.54	0.93	1.24	1.17	1.21
3'(2'),5'-bisphosphate nucleotidase 1 isoform 2 [Homo sapiens]	2.54	0.93	1.24	1.17	1.21
solute carrier family 2, facilitated glucose transporter member 14 isoform a [Homo sapiens]	0.52	1.62	1.74	0.71	0.64
translationally-controlled tumor protein isoform 3 [Homo sapiens]	1.31	1.24	3.23	3.95	1.94
solute carrier family 2, facilitated glucose transporter member 14 isoform c [Homo sapiens]	0.52	1.62	1.74	0.71	0.64

solute carrier family 2, facilitated glucose transporter member 14 isoform b [Homo sapiens]	0.52	1.62	1.74	0.71	0.64
solute carrier family 2, facilitated glucose transporter member 14 isoform d [Homo sapiens]	0.52	1.62	1.74	0.71	0.64
translationally-controlled tumor protein isoform 1 [Homo sapiens]	1.28	1.28	2.68	3.39	1.94
hydroxyacylglutathione hydrolase, mitochondrial isoform 3 precursor [Homo sapiens]	85.95	1.00	1.69	1.63	1.40
vacuolar protein sorting-associated protein VTA1 homolog isoform c [Homo sapiens]	2.83	1.51	1.87	1.31	1.55
vacuolar protein sorting-associated protein VTA1 homolog isoform b [Homo sapiens]	2.83	1.51	1.87	1.31	1.55
integrin alpha-X isoform 1 precursor [Homo sapiens]	0.31	1.21	0.68	0.41	0.71
protein FAM65B isoform 5 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
protein FAM65B isoform 4 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
protein FAM65B isoform 3 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
eukaryotic translation initiation factor 3 subunit C isoform b [Homo sapiens]	5.56	1.25	1.27	1.30	1.24
heat shock protein 105 kDa isoform 2 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
heat shock protein 105 kDa isoform 4 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
heat shock protein 105 kDa isoform 3 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
NEDD8-activating enzyme E1 regulatory subunit isoform d [Homo sapiens]	2.34	1.22	1.37	1.64	1.20
SAM domain-containing protein SAMSN-1 isoform 3 [Homo sapiens]	0.52	0.91	0.79	0.85	0.83
protein-methionine sulfoxide oxidase MICAL1 isoform 3 [Homo sapiens]	0.67	1.19	2.29	1.74	1.88
periostin isoform 6 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
periostin isoform 5 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
periostin isoform 7 precursor [Homo sapiens]	0.91	0.82	0.66	0.23	1.81
ubiquitin-fold modifier 1 isoform 4 [Homo sapiens]	1.31	0.63	0.61	0.58	0.67
ubiquitin-fold modifier 1 isoform 2 [Homo sapiens]	1.31	0.63	0.61	0.58	0.67
long-chain-fatty-acid--CoA ligase 1 isoform b [Homo sapiens]	0.69	1.35	1.60	1.56	0.82
long-chain-fatty-acid--CoA ligase 1 isoform c [Homo sapiens]	0.69	1.35	1.60	1.56	0.82
long-chain-fatty-acid--CoA ligase 1 isoform d [Homo sapiens]	0.67	1.29	0.94	1.73	0.96
carbonyl reductase [NADPH] 1 isoform 2 [Homo sapiens]	0.98	0.94	0.57	0.46	0.74
nicotinate phosphoribosyltransferase isoform 2 [Homo sapiens]	2.31	1.51	1.21	0.98	1.00
protein PRRC1 isoform 1 [Homo sapiens]	3.52	1.74	3.23	3.34	2.11
tumor necrosis factor alpha-induced protein 8 isoform d [Homo sapiens]	2.79	4.73	1.34	0.99	1.26
tumor necrosis factor alpha-induced protein 8 isoform c [Homo sapiens]	2.79	4.73	1.34	0.99	1.26
Golgi-associated plant pathogenesis-related protein 1 isoform b [Homo sapiens]	0.83	0.98	1.96	2.77	2.68
Golgi-associated plant pathogenesis-related protein 1 isoform f [Homo sapiens]	2.38	1.73	2.16	1.25	1.20
Golgi-associated plant pathogenesis-related protein 1 isoform c [Homo sapiens]	0.57	0.79	0.84	0.75	0.88
Golgi-associated plant pathogenesis-related protein 1 isoform e [Homo sapiens]	0.66	0.91	1.78	2.55	1.94
FYVE, RhoGEF and PH domain-containing protein 3 isoform b [Homo sapiens]	0.88	0.89	1.22	1.52	0.78
actin-related protein 2/3 complex subunit 3 isoform 2 [Homo sapiens]	0.95	1.21	2.49	2.74	1.30
RNA-binding Raly-like protein isoform 3 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35
calcium-binding protein 39-like [Homo sapiens]	0.46	1.40	1.90	2.80	1.42

tyrosine-protein kinase BTK isoform 3 [Homo sapiens]	0.39	0.79	0.31	0.18	0.53
tyrosine-protein kinase BTK isoform 2 [Homo sapiens]	0.39	0.79	0.31	0.18	0.53
rho GTPase-activating protein 30 isoform 4 [Homo sapiens]	0.10	1.17	2.29	1.78	0.98
protein SETSIP [Homo sapiens]	1.24	2.18	4.08	4.06	2.80
chloride intracellular channel protein 1 [Homo sapiens]	0.91	0.91	1.44	1.44	1.23
cytoplasmic FMR1-interacting protein 1 isoform a [Homo sapiens]	1.89	0.98	2.45	5.66	1.87
BRO1 domain-containing protein BROX isoform c [Homo sapiens]	2.49	1.51	1.36	1.22	1.88
BRO1 domain-containing protein BROX isoform b [Homo sapiens]	1.61	0.88	0.94	0.79	0.90
hematological and neurological expressed 1 protein isoform 3 [Homo sapiens]	0.39	0.82	1.72	2.27	0.53
cystatin-C precursor [Homo sapiens]	2.79	1.65	0.62	0.38	0.74
hematological and neurological expressed 1 protein isoform 4 [Homo sapiens]	0.39	0.82	1.72	2.27	0.53
clathrin heavy chain 1 isoform 2 [Homo sapiens]	1.76	0.85	0.90	2.01	0.78
signal transducer and activator of transcription 5A isoform 2 [Homo sapiens]	0.45	0.68	1.19	1.98	0.76
signal transducer and activator of transcription 5A isoform 3 [Homo sapiens]	0.45	0.68	1.19	1.98	0.76
dynamin-1 isoform 3 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
dynamin-1 isoform 4 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
BRISC and BRCA1-A complex member 1 isoform 2 [Homo sapiens]	1.61	2.52	2.56	4.18	2.74
X-ray repair cross-complementing protein 6 isoform 2 [Homo sapiens]	1.24	1.62	2.47	0.98	2.39
X-ray repair cross-complementing protein 6 isoform 3 [Homo sapiens]	1.34	1.62	1.96	1.33	2.08
kallistatin isoform 1 [Homo sapiens]	0.52	0.49	0.20	0.14	0.49
kallistatin isoform 2 precursor [Homo sapiens]	0.52	0.49	0.20	0.14	0.49
histidine--tRNA ligase, cytoplasmic isoform 5 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
histidine--tRNA ligase, cytoplasmic isoform 6 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
histidine--tRNA ligase, cytoplasmic isoform 7 [Homo sapiens]	2.38	1.00	1.38	1.92	1.26
glucosidase 2 subunit beta isoform 2 precursor [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
glucosidase 2 subunit beta isoform 3 precursor [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
copine-4 isoform 1 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
dihydrolipoyl dehydrogenase, mitochondrial isoform 2 [Homo sapiens]	0.75	1.21	1.76	1.42	1.48
dihydrolipoyl dehydrogenase, mitochondrial isoform 3 [Homo sapiens]	0.75	1.21	1.76	1.42	1.48
glucose-6-phosphate isomerase isoform 3 [Homo sapiens]	0.88	1.27	1.47	1.45	1.44
glucose-6-phosphate isomerase isoform 4 [Homo sapiens]	0.80	1.27	1.62	1.45	1.44
pterin-4-alpha-carbinolamine dehydratase isoform 3 [Homo sapiens]	0.80	0.92	0.71	0.49	0.76
PREDICTED: 40S ribosomal protein S8-like [Homo sapiens]	0.35	0.64	0.37	0.44	0.50
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	1.79	0.73	0.57	0.28	0.88
PREDICTED: ES1 protein homolog, mitochondrial-like isoform X1 [Homo sapiens]	0.46	0.81	0.94	0.42	0.76
PREDICTED: ES1 protein homolog, mitochondrial-like isoform X3 [Homo sapiens]	0.46	0.81	0.94	0.42	0.76

PREDICTED: uncharacterized protein LOC100293211 [Homo sapiens]	0.35	0.77	0.33	0.16	0.66
PREDICTED: myosin light chain kinase 2, skeletal/cardiac muscle-like [Homo sapiens]	0.95	0.77	0.68	0.52	0.81
PREDICTED: signal-regulatory protein beta-1 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like, partial [Homo sapiens]	0.57	1.25	0.90	1.97	1.57
PREDICTED: putative trypsin-6-like [Homo sapiens]	1.61	0.48	0.20	0.13	0.32
PREDICTED: low affinity immunoglobulin gamma Fc region receptor III-A-like isoform X2 [Homo sapiens]	0.54	2.31	1.74	2.45	7.01
PREDICTED: adenyl cyclase-associated protein 1 isoform X3 [Homo sapiens]	0.62	1.27	1.87	1.99	1.42
PREDICTED: oxysterol-binding protein-related protein 9 isoform X1 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: oxysterol-binding protein-related protein 9 isoform X2 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: oxysterol-binding protein-related protein 9 isoform X3 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: oxysterol-binding protein-related protein 9 isoform X4 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: oxysterol-binding protein-related protein 9 isoform X5 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: oxysterol-binding protein-related protein 9 isoform X9 [Homo sapiens]	0.56	0.87	0.79	2.81	0.97
PREDICTED: calponin-3 isoform X1 [Homo sapiens]	0.91	0.79	0.95	1.66	1.47
PREDICTED: dihydropyrimidine dehydrogenase [NADP(+)] isoform X2 [Homo sapiens]	0.80	0.94	1.43	0.91	0.81
PREDICTED: dihydropyrimidine dehydrogenase [NADP(+)] isoform X3 [Homo sapiens]	0.80	0.94	1.43	0.91	0.81
PREDICTED: alpha-enolase isoform X1 [Homo sapiens]	0.88	1.27	1.43	1.41	1.28
PREDICTED: protein 4.1 isoform X23 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X24 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X25 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X26 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X27 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X28 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: protein 4.1 isoform X29 [Homo sapiens]	3.75	0.77	0.40	0.20	0.55
PREDICTED: epidermal growth factor receptor substrate 15 isoform X3 [Homo sapiens]	0.62	1.40	1.37	1.35	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X6 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X7 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X8 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X9 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X10 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X11 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X12 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X13 [Homo sapiens]	1.64	1.24	0.66	0.67	0.88
PREDICTED: AMP deaminase 2 isoform X2 [Homo sapiens]	1.34	0.88	0.66	0.75	0.91
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X6 [Homo sapiens]	1.37	4.07	2.56	0.83	3.52
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X7 [Homo sapiens]	1.37	4.07	2.56	0.83	3.52

sapiens]					
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X8 [Homo sapiens]	1.37	4.07	2.56	0.83	3.52
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X9 [Homo sapiens]	1.37	4.07	2.56	0.83	3.52
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X10 [Homo sapiens]	1.24	9.50	1.87	1.35	5.57
PREDICTED: protein-arginine deiminase type-3 isoform X1 [Homo sapiens]	0.88	0.82	0.50	0.87	0.96
PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform isoform X6 [Homo sapiens]	2.02	0.76	2.47	1.54	0.89
PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform isoform X7 [Homo sapiens]	2.02	0.76	2.47	1.54	0.89
PREDICTED: cAMP-dependent protein kinase catalytic subunit beta isoform X10 [Homo sapiens]	0.80	0.71	0.55	0.60	0.66
PREDICTED: serine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	1.64	0.76	0.53	0.48	0.67
PREDICTED: centrosomal protein of 85 kDa isoform X3 [Homo sapiens]	732.97	0.96	3.92	0.88	2.50
PREDICTED: nicotinamide mononucleotide adenylyltransferase 1 isoform X3 [Homo sapiens]	1.82	2.46	1.28	0.77	1.60
PREDICTED: NAD kinase isoform X5 [Homo sapiens]	2.27	0.97	2.29	1.22	2.16
PREDICTED: NAD kinase isoform X6 [Homo sapiens]	2.27	0.97	2.29	1.22	2.16
PREDICTED: complement component C8 beta chain isoform X2 [Homo sapiens]	0.33	2.08	0.53	0.31	0.52
PREDICTED: F-actin-capping protein subunit beta isoform X1 [Homo sapiens]	0.66	1.40	1.34	1.70	1.94
PREDICTED: far upstream element-binding protein 1 isoform X2 [Homo sapiens]	0.77	0.77	0.98	0.82	2.60
PREDICTED: far upstream element-binding protein 1 isoform X3 [Homo sapiens]	0.77	0.77	0.98	0.82	2.60
PREDICTED: heterogeneous nuclear ribonucleoprotein C-like 1-like [Homo sapiens]	0.98	2.45	1.63	3.87	1.62
PREDICTED: proteoglycan 4 isoform X2 [Homo sapiens]	0.54	2.32	0.70	0.41	0.79
PREDICTED: proteoglycan 4 isoform X1 [Homo sapiens]	0.54	2.32	0.70	0.41	0.79
PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1 isoform X9 [Homo sapiens]	2.54	0.93	1.24	1.17	1.21
PREDICTED: complement factor H-related protein 4 isoform X1 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X2 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X3 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X4 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X5 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement factor H-related protein 4 isoform X7 [Homo sapiens]	2.19	2.16	1.55	0.85	1.72
PREDICTED: complement receptor type 1 isoform X2 [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
PREDICTED: complement receptor type 1 isoform X3 [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
PREDICTED: complement receptor type 1 isoform X4 [Homo sapiens]	0.69	2.08	0.66	0.41	0.76
PREDICTED: BRO1 domain-containing protein BROX isoform X6 [Homo sapiens]	1.76	1.00	1.27	1.21	0.92

PREDICTED: protein crumbs homolog 1 isoform X1 [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
PREDICTED: protein crumbs homolog 1 isoform X2 [Homo sapiens]	1.54	0.62	0.30	0.20	0.49
PREDICTED: dynamin-3 isoform X7 [Homo sapiens]	0.64	0.85	0.62	0.63	0.76
PREDICTED: hepatoma-derived growth factor isoform X1 [Homo sapiens]	2.79	1.35	1.46	2.30	1.50
PREDICTED: hepatoma-derived growth factor isoform X2 [Homo sapiens]	1.31	1.36	1.46	1.81	1.80
PREDICTED: complement factor H isoform X1 [Homo sapiens]	0.39	0.99	0.58	0.30	0.74
PREDICTED: complement factor H isoform X2 [Homo sapiens]	0.39	0.99	0.57	0.29	0.73
PREDICTED: complement factor H-related protein 1 isoform X1 [Homo sapiens]	0.31	1.62	0.67	0.43	0.70
PREDICTED: complement factor H-related protein 2 isoform X2 [Homo sapiens]	0.41	2.20	0.77	0.25	0.70
PREDICTED: protein S100-A7A isoform X1 [Homo sapiens]	3.26	0.93	1.39	0.55	6.20
PREDICTED: gamma-interferon-inducible protein 16 isoform X2 [Homo sapiens]	0.35	0.64	0.33	0.30	0.44
PREDICTED: histone H2B type 2-F isoform X1 [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
PREDICTED: histone H2B type 2-F isoform X2 [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X9 [Homo sapiens]	0.41	0.99	2.68	1.73	1.27
PREDICTED: nitrilase homolog 1 isoform X4 [Homo sapiens]	2.19	0.92	0.75	0.56	0.81
PREDICTED: pyruvate kinase PKLR isoform X2 [Homo sapiens]	0.43	0.87	1.78	1.72	1.27
PREDICTED: receptor-type tyrosine-protein phosphatase C isoform X1 [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
PREDICTED: receptor-type tyrosine-protein phosphatase C isoform X2 [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
PREDICTED: receptor-type tyrosine-protein phosphatase C isoform X3 [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
PREDICTED: receptor-type tyrosine-protein phosphatase C isoform X4 [Homo sapiens]	0.66	1.44	1.71	1.36	1.35
PREDICTED: 60 kDa SS-A/Ro ribonucleoprotein isoform X1 [Homo sapiens]	0.66	1.42	1.86	1.51	1.54
PREDICTED: 60 kDa SS-A/Ro ribonucleoprotein isoform X3 [Homo sapiens]	0.66	1.42	1.86	1.51	1.54
PREDICTED: tropomyosin alpha-3 chain isoform X1 [Homo sapiens]	0.52	1.19	2.49	1.76	1.30
PREDICTED: tropomyosin alpha-3 chain isoform X2 [Homo sapiens]	0.52	1.19	2.49	1.76	1.30
PREDICTED: tropomyosin alpha-3 chain isoform X3 [Homo sapiens]	0.52	1.19	2.49	1.76	1.30
PREDICTED: tropomyosin alpha-3 chain isoform X5 [Homo sapiens]	1.34	1.21	1.91	5.18	1.71
PREDICTED: tropomyosin alpha-3 chain isoform X6 [Homo sapiens]	0.52	1.19	2.49	1.76	1.30
PREDICTED: tropomyosin alpha-3 chain isoform X7 [Homo sapiens]	1.34	1.21	1.91	5.18	1.71
PREDICTED: tropomyosin alpha-3 chain isoform X9 [Homo sapiens]	1.31	1.62	0.90	0.89	0.92
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X10 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: rho guanine nucleotide exchange factor 2 isoform X14 [Homo sapiens]	0.50	1.90	0.88	1.46	2.01
PREDICTED: zinc finger CCCH domain-containing protein 11A isoform X6 [Homo sapiens]		0.43	0.51	1.37	0.50
PREDICTED: protein disulfide-isomerase A6 isoform X4 [Homo sapiens]	2.79	1.59	2.26	1.79	1.56
PREDICTED: hippocalcin-like protein 1 isoform X5	1.71	1.00	1.59	3.12	1.59

[Homo sapiens]

PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	1.31	1.90	2.68	2.33	1.63
PREDICTED: microtubule-associated protein RP/EB family member 3 isoform X1 [Homo sapiens]	1.71	0.96	1.42	1.93	1.26
PREDICTED: echinoderm microtubule-associated protein-like 4 isoform X3 [Homo sapiens]	1.28	1.28	1.43	1.30	1.25
PREDICTED: echinoderm microtubule-associated protein-like 4 isoform X4 [Homo sapiens]	1.28	1.53	1.87	1.25	1.54
PREDICTED: annexin A4 isoform X1 [Homo sapiens]	2.17	1.57	1.55	2.13	1.90
PREDICTED: EKC/KEOPS complex subunit TPRKB isoform X5 [Homo sapiens]	20.02	1.30	1.24	2.77	1.00
PREDICTED: N-acetyl-D-glucosamine kinase isoform X5 [Homo sapiens]	0.64	0.85	0.85	0.83	1.18
PREDICTED: UTP--glucose-1-phosphate uridylyltransferase isoform X4 [Homo sapiens]	2.79	2.20	1.24	1.41	1.00
PREDICTED: exportin-1 isoform X5 [Homo sapiens]	5.15	1.96	0.77	0.95	0.92
PREDICTED: exportin-1 isoform X7 [Homo sapiens]	5.15	1.96	0.77	0.95	0.92
PREDICTED: lymphocyte-specific protein 1-like [Homo sapiens]	0.98	0.98	0.65	0.80	0.93
PREDICTED: actin-related protein 2/3 complex subunit 2 isoform X1 [Homo sapiens]	0.77	1.21	1.62	1.60	1.18
PREDICTED: serine/threonine-protein kinase 25 isoform X1 [Homo sapiens]	1.54	1.30	1.65	1.39	1.61
PREDICTED: collagen alpha-3(VI) chain isoform X3 [Homo sapiens]	2.15	1.79	0.52	0.32	0.90
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X8 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X9 [Homo sapiens]	0.62	0.85	1.51	1.68	0.98
PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X4 [Homo sapiens]	0.77	0.97	1.34	1.75	1.34
PREDICTED: grancalcin isoform X2 [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
PREDICTED: grancalcin isoform X3 [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
PREDICTED: grancalcin isoform X4 [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
PREDICTED: grancalcin isoform X5 [Homo sapiens]	1.37	1.69	2.01	3.37	2.51
PREDICTED: myc box-dependent-interacting protein 1 isoform X8 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X9 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X10 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X11 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X12 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X13 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X14 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X15 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X16 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X17 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: myc box-dependent-interacting protein 1 isoform X18 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: bifunctional purine biosynthesis protein PURH isoform X1 [Homo sapiens]	9.83	2.08	1.18	1.74	1.44
PREDICTED: septin-2 isoform X6 [Homo sapiens]	3.39	1.51	2.69	0.59	0.87
PREDICTED: septin-2 isoform X7 [Homo sapiens]	3.39	1.51	2.69	0.59	0.87
PREDICTED: dedicator of cytokinesis protein 10	0.26	2.19	1.34	0.54	1.61

isoform X4 [Homo sapiens]					
PREDICTED: dedicator of cytokinesis protein 10 isoform X5 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X6 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X7 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X8 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X9 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X10 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X11 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: dedicator of cytokinesis protein 10 isoform X12 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
PREDICTED: pre-mRNA-processing factor 40 homolog A isoform X2 [Homo sapiens]	0.33	0.92	1.46	2.49	1.57
PREDICTED: pre-mRNA-processing factor 40 homolog A isoform X3 [Homo sapiens]	0.33	0.92	1.46	2.49	1.57
PREDICTED: rho GTPase-activating protein 15 isoform X2 [Homo sapiens]	1.18	2.45	1.72	2.14	1.28
PREDICTED: vitamin K-dependent protein C isoform X4 [Homo sapiens]	0.43	0.43	0.30	0.13	0.23
PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X1 [Homo sapiens]	0.95	1.29	1.26	1.30	0.85
PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X2 [Homo sapiens]	0.95	1.29	1.26	1.30	0.85
PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform X3 [Homo sapiens]	0.95	1.29	1.26	1.30	0.85
PREDICTED: ribulose-phosphate 3-epimerase isoform X1 [Homo sapiens]	0.39	0.62	0.61	0.62	0.74
PREDICTED: COP9 signalosome complex subunit 7b isoform X1 [Homo sapiens]	7.95	0.57	0.60	0.57	0.42
PREDICTED: cullin-3 isoform X1 [Homo sapiens]	1.00	0.94	0.62	0.66	0.51
PREDICTED: serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B isoform X5 [Homo sapiens]	0.26	1.96	0.88	1.37	0.76
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X32 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X33 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X34 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X35 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X36 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X37 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X38 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X39 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X40 [Homo sapiens]	0.57	1.30	0.95	0.95	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X41 [Homo sapiens]	0.57	1.00	0.88	0.80	0.74
PREDICTED: leucine-rich repeat flightless-interacting protein 1 isoform X42 [Homo sapiens]	3.70	2.59	0.75	0.57	0.88
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X11 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: E3 ubiquitin-protein ligase TRIP12 isoform X12 [Homo sapiens]	0.31	1.18	1.36	1.64	0.99
PREDICTED: ubiquitin-like modifier-activating enzyme	0.80	0.91	0.82	0.98	0.92

ATG7 isoform X7 [Homo sapiens]					
PREDICTED: ubiquitin-like modifier-activating enzyme					
ATG7 isoform X8 [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
PREDICTED: ubiquitin-like modifier-activating enzyme					
ATG7 isoform X9 [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
PREDICTED: ubiquitin-like modifier-activating enzyme					
ATG7 isoform X10 [Homo sapiens]	0.80	0.91	0.82	0.98	0.92
PREDICTED: potassium voltage-gated channel subfamily H member					
8 isoform X1 [Homo sapiens]		2.71	3.23	3.11	1.44
PREDICTED: potassium voltage-gated channel subfamily H member					
8 isoform X2 [Homo sapiens]		2.71	3.23	3.11	1.44
PREDICTED: potassium voltage-gated channel subfamily H member					
8 isoform X3 [Homo sapiens]		2.71	3.23	3.11	1.44
PREDICTED: potassium voltage-gated channel subfamily H member					
8 isoform X4 [Homo sapiens]		2.71	3.23	3.11	1.44
PREDICTED: filamin-B isoform X7 [Homo sapiens]	0.77	0.83	0.81	0.75	0.93
PREDICTED: neurobeachin-like protein 2 isoform X5					
[Homo sapiens]	1.64	0.74	0.56	0.64	0.61
PREDICTED: inosine-5'-monophosphate					
dehydrogenase 2 isoform X1 [Homo sapiens]	1.00	0.81	0.77	1.98	0.82
PREDICTED: inter-alpha-trypsin inhibitor heavy chain					
H3 isoform X2 [Homo sapiens]	0.67	1.26	0.80	0.44	2.34
PREDICTED: inter-alpha-trypsin inhibitor heavy chain					
H3 isoform X3 [Homo sapiens]	0.67	1.25	0.79	0.43	2.16
PREDICTED: hepatocyte growth factor-like protein					
isoform X1 [Homo sapiens]	0.56	0.81	0.46	0.29	0.66
PREDICTED: hepatocyte growth factor-like protein					
isoform X2 [Homo sapiens]	0.56	0.73	0.53	0.29	0.68
PREDICTED: hepatocyte growth factor-like protein					
isoform X3 [Homo sapiens]	0.56	0.81	0.53	0.29	0.68
PREDICTED: hepatocyte growth factor-like protein					
isoform X4 [Homo sapiens]	0.56	0.73	0.53	0.29	0.68
PREDICTED: protein kinase C delta type isoform X1					
[Homo sapiens]	0.95	0.69	0.88	1.37	0.73
PREDICTED: protein kinase C delta type isoform X2					
[Homo sapiens]	0.95	0.69	0.88	1.37	0.73
PREDICTED: protein SEC13 homolog isoform X4					
[Homo sapiens]	1.31	1.19	0.79	0.82	0.89
PREDICTED: protein SEC13 homolog isoform X6					
[Homo sapiens]	1.31	1.19	0.79	0.82	0.89
PREDICTED: biotinidase isoform X5 [Homo sapiens]	0.06	0.49	0.17	0.13	0.24
PREDICTED: transketolase isoform X1 [Homo sapiens]	0.64	1.24	1.72	1.00	1.43
PREDICTED: ubiquitin-like modifier-activating enzyme					
7 isoform X3 [Homo sapiens]	0.39	0.88	0.88	0.89	1.28
PREDICTED: calcium-dependent secretion activator 1 isoform X1					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X2					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X3					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X4					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X5					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X6					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X7					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X8					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X9					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X10					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X11					
		0.78	1.44	0.15	0.17

[Homo sapiens]					
PREDICTED: calcium-dependent secretion activator 1 isoform X12					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X13					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X14					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X15					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X16					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: calcium-dependent secretion activator 1 isoform X17					
[Homo sapiens]		0.78	1.44	0.15	0.17
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X21 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X22 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X23 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X24 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X26 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X27 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X28 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X29 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X30 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X31 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X32 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X33 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X34 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X35 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X36 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X38 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X39 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: leucine-rich repeat flightless-interacting protein 2 isoform X40 [Homo sapiens]	3.47	1.25	1.43	1.21	1.54
PREDICTED: ceruloplasmin isoform X1 [Homo sapiens]	0.56	1.24	0.52	0.32	0.85
PREDICTED: ceruloplasmin isoform X2 [Homo sapiens]	0.56	1.24	0.52	0.32	0.85
PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]	0.56	1.24	0.52	0.32	0.85
PREDICTED: ceruloplasmin isoform X4 [Homo sapiens]	0.50	1.22	0.52	0.32	0.90
PREDICTED: arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 isoform X1 [Homo sapiens]	2.79	0.94	0.79	0.64	0.76
PREDICTED: arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 isoform X2 [Homo sapiens]	2.79	0.94	0.79	0.64	0.76
PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform X3 [Homo sapiens]	0.28	0.93	1.21	2.77	0.84
PREDICTED: WD repeat-containing protein 1 isoform X1 [Homo sapiens]	1.64	1.00	1.46	0.88	1.50
PREDICTED: phosphoglucomutase-2 isoform X1 [Homo sapiens]	1.41	1.19	2.76	1.41	1.29

PREDICTED: multifunctional protein ADE2 isoform X1 [Homo sapiens]	3.12	1.96	1.59	1.96	1.46
PREDICTED: afamin isoform X1 [Homo sapiens]	0.35	0.58	0.23	0.12	0.41
PREDICTED: eukaryotic translation initiation factor 4E isoform X1 [Homo sapiens]	5.87	1.26	2.15	3.30	1.30
PREDICTED: eukaryotic translation initiation factor 4E isoform X2 [Homo sapiens]	5.87	1.26	2.15	3.30	1.30
PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	0.33	1.30	0.69	0.30	0.81
PREDICTED: long-chain-fatty-acid--CoA ligase 1 isoform X6 [Homo sapiens]	0.69	1.35	1.60	1.56	0.82
PREDICTED: vitamin D-binding protein isoform X1 [Homo sapiens]	0.31	0.93	0.48	0.28	0.57
PREDICTED: complement factor I isoform X3 [Homo sapiens]	0.43	1.51	0.58	0.31	0.69
PREDICTED: complement factor I isoform X4 [Homo sapiens]	0.43	1.51	0.58	0.33	0.70
PREDICTED: immunoglobulin J chain isoform X2 [Homo sapiens]	0.66	1.00	0.46	0.25	1.20
PREDICTED: plasma kallikrein isoform X2 [Homo sapiens]	0.33	0.62	0.29	0.18	0.43
PREDICTED: nuclear factor NF-kappa-B p105 subunit isoform X2 [Homo sapiens]	1.96	0.55	0.40	0.24	0.44
PREDICTED: ubiquitin-like modifier-activating enzyme 6 isoform X1 [Homo sapiens]	0.69	0.91	2.16	1.19	0.99
PREDICTED: septin-11 isoform X4 [Homo sapiens]	1.24	0.92	1.34	1.18	1.74
PREDICTED: mitogen-activated protein kinase 10 isoform X14 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: mitogen-activated protein kinase 10 isoform X15 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: mitogen-activated protein kinase 10 isoform X17 [Homo sapiens]	4.19	2.05	4.38	5.01	2.08
PREDICTED: ubiquitin-conjugating enzyme E2 D3 isoform X10 [Homo sapiens]	1.31	0.85	1.21	1.24	0.96
PREDICTED: general vesicular transport factor p115 isoform X2 [Homo sapiens]	3.17	1.26	0.48	0.46	0.57
PREDICTED: general vesicular transport factor p115 isoform X3 [Homo sapiens]	0.66	0.93	0.67	0.70	0.74
PREDICTED: MOB kinase activator 1B isoform X2 [Homo sapiens]	1.71	0.96	1.29	1.44	0.94
PREDICTED: FYN-binding protein isoform X1 [Homo sapiens]	1.71	1.63	0.81	0.79	0.94
PREDICTED: complement component C6 isoform X3 [Homo sapiens]	0.33	1.90	0.64	0.33	0.67
PREDICTED: complement component C6 isoform X4 [Homo sapiens]	0.33	1.30	0.60	0.32	0.57
PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X7 [Homo sapiens]	1.18	1.30	1.54	1.57	0.96
PREDICTED: protein PRRC1 isoform X1 [Homo sapiens]	3.52	1.74	3.23	3.34	2.11
PREDICTED: tumor necrosis factor alpha-induced protein 8 isoform X1 [Homo sapiens]	2.79	4.73	1.34	0.99	1.26
PREDICTED: uncharacterized protein KIAA0825 isoform X1 [Homo sapiens]	0.35	0.69	0.31	0.18	0.49
PREDICTED: calpastatin isoform X1 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X2 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X3 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X4 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X5 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X6 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X7 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X8 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X9 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23

PREDICTED: calpastatin isoform X10 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X11 [Homo sapiens]	3.86	1.30	1.68	1.61	1.23
PREDICTED: calpastatin isoform X12 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X13 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X14 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X15 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X16 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X17 [Homo sapiens]	10.27	0.98	1.39	1.42	0.99
PREDICTED: calpastatin isoform X18 [Homo sapiens]	12.11	2.08	1.39	1.42	0.99
PREDICTED: calpastatin isoform X19 [Homo sapiens]	12.11	2.08	1.39	1.42	0.99
PREDICTED: calpastatin isoform X20 [Homo sapiens]	12.11	2.08	1.39	1.42	0.99
PREDICTED: probable histidine--tRNA ligase, mitochondrial isoform X1 [Homo sapiens]	4.55	1.00	1.26	1.44	2.76
PREDICTED: probable histidine--tRNA ligase, mitochondrial isoform X2 [Homo sapiens]	4.55	1.00	1.26	1.44	2.76
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X14 [Homo sapiens]	0.18	0.68	0.21	0.08	0.41
PREDICTED: eukaryotic translation initiation factor 4E type 1B isoform X1 [Homo sapiens]	8.36	1.51	3.57	5.72	1.88
PREDICTED: G protein-coupled receptor kinase 6 isoform X1 [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
PREDICTED: G protein-coupled receptor kinase 6 isoform X2 [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
PREDICTED: G protein-coupled receptor kinase 6 isoform X3 [Homo sapiens]	0.39	1.25	0.74	1.21	1.35
PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X10 [Homo sapiens]	4.84	1.69	2.26	3.89	1.47
PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X11 [Homo sapiens]	4.84	1.69	2.26	3.89	1.47
PREDICTED: nucleophosmin isoform X3 [Homo sapiens]	1.00	1.51	1.44	0.65	1.36
PREDICTED: beta-synuclein isoform X1 [Homo sapiens]	49.47	0.70	0.64	0.35	0.80
PREDICTED: beta-synuclein isoform X3 [Homo sapiens]	49.47	0.70	0.64	0.35	0.80
PREDICTED: docking protein 3 isoform X6 [Homo sapiens]	0.91	0.80	0.48	0.52	0.68
PREDICTED: protein canopy homolog 3 isoform X5 [Homo sapiens]	1.28	2.32	0.78	0.46	0.83
PREDICTED: mitogen-activated protein kinase 14 isoform X1 [Homo sapiens]	2.19	2.45	1.40	1.34	1.94
PREDICTED: leukocyte elastase inhibitor isoform X1 [Homo sapiens]	0.66	1.42	1.62	1.75	1.82
PREDICTED: GDP-mannose 4,6 dehydratase isoform X1 [Homo sapiens]	2.38	1.40	1.40	1.24	1.17
PREDICTED: serpin B6 isoform X4 [Homo sapiens]	1.54	2.71	1.19	0.96	2.68
PREDICTED: copine-5 isoform X9 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: copine-5 isoform X10 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: protein FAM65B isoform X1 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
PREDICTED: protein FAM65B isoform X2 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
PREDICTED: protein FAM65B isoform X6 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
PREDICTED: protein FAM65B isoform X7 [Homo sapiens]	0.13	0.44	0.88	0.45	0.84
PREDICTED: KH domain-containing, RNA-binding, signal transduction-associated protein 2 isoform X1 [Homo sapiens]	0.45	1.25	2.57	3.85	1.93
PREDICTED: KH domain-containing, RNA-binding, signal transduction-associated protein 2 isoform X2	0.45	1.25	2.57	3.85	1.93

[Homo sapiens]

PREDICTED: SAM and SH3 domain-containing protein 1 isoform X3 [Homo sapiens]	0.52	0.91	0.79	0.85	0.83
PREDICTED: nesprin-1 isoform X1 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X2 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X3 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X4 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X5 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X6 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X7 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X8 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X9 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X10 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X11 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X12 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X14 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X15 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X16 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X17 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X18 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: nesprin-1 isoform X19 [Homo sapiens]	1.96	0.74	0.63	0.98	0.70
PREDICTED: ezrin isoform X1 [Homo sapiens]	1.34	1.62	1.39	1.64	1.23
PREDICTED: vascular non-inflammatory molecule 2 isoform X1 [Homo sapiens]	0.50	0.80	0.43	0.29	0.78
PREDICTED: glycine--tRNA ligase isoform X1 [Homo sapiens]	0.88	0.93	0.95	0.65	2.34
PREDICTED: amphiphysin isoform X1 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: amphiphysin isoform X2 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: amphiphysin isoform X3 [Homo sapiens]	0.28	0.92	0.52	0.52	0.79
PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]	0.80	0.95	1.30	1.61	1.23
PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	2.38	1.21	0.82	1.26	0.96
PREDICTED: septin-7 isoform X1 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
PREDICTED: septin-7 isoform X2 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
PREDICTED: septin-7 isoform X3 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
PREDICTED: septin-7 isoform X4 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
PREDICTED: septin-7 isoform X5 [Homo sapiens]	0.69	1.40	1.51	1.63	2.60
PREDICTED: actin-related protein 2/3 complex subunit 1B isoform X2 [Homo sapiens]	0.57	1.26	1.48	1.75	1.42
PREDICTED: filamin-C isoform X1 [Homo sapiens]	0.62	1.73	2.54	3.82	2.24
PREDICTED: transportin-3 isoform X1 [Homo sapiens]	1.31	0.77	0.57	0.79	0.58
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X3 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X4 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X5 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X6 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X7 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X8 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76
PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform X9 [Homo sapiens]	0.43	0.75	0.69	0.91	0.76

PREDICTED: actin-like protein 6B isoform X1 [Homo sapiens]	0.45	2.07	3.60	3.63	1.81
PREDICTED: trypsin-2 isoform X2 [Homo sapiens]	1.61	0.48	0.20	0.13	0.32
PREDICTED: actin-related protein 3B isoform X1 [Homo sapiens]	1.24	1.26	1.77	2.19	1.37
PREDICTED: actin-related protein 3B isoform X2 [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
PREDICTED: actin-related protein 3B isoform X3 [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
PREDICTED: actin-related protein 3B isoform X4 [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
PREDICTED: actin-related protein 3B isoform X5 [Homo sapiens]	1.24	1.26	1.77	2.19	1.37
PREDICTED: neutrophil cytosol factor 1 isoform X1 [Homo sapiens]	0.83	0.63	0.85	1.34	1.35
PREDICTED: neutrophil cytosol factor 1 isoform X2 [Homo sapiens]	0.91	0.64	0.85	1.36	1.35
PREDICTED: actin-related protein 3C isoform X1 [Homo sapiens]	1.37	1.29	1.79	2.12	1.37
PREDICTED: sorcin isoform X1 [Homo sapiens]	14.12	0.75	0.66	0.69	1.61
PREDICTED: maltase-glucoamylase, intestinal isoform X2 [Homo sapiens]	21.72	0.93	0.54	0.35	0.58
PREDICTED: protein disulfide-isomerase A4 isoform X1 [Homo sapiens]	0.80	1.41	2.07	1.54	1.57
PREDICTED: clusterin isoform X1 [Homo sapiens]	0.26	0.52	0.30	0.14	0.40
PREDICTED: acyl-protein thioesterase 1 isoform X2 [Homo sapiens]	0.80	0.79	0.82	0.99	0.90
PREDICTED: RNA-binding Raly-like protein isoform X2 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35
PREDICTED: RNA-binding Raly-like protein isoform X3 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35
PREDICTED: RNA-binding Raly-like protein isoform X6 [Homo sapiens]	2.79	0.79	1.48	4.80	1.35
PREDICTED: elongation factor 1-delta isoform X8 [Homo sapiens]	0.25	0.83	0.71	0.44	0.67
PREDICTED: protein FAM49B isoform X5 [Homo sapiens]	0.98	0.92	0.90	1.21	1.88
PREDICTED: plectin isoform X10 [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
PREDICTED: plectin isoform X11 [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
PREDICTED: plectin isoform X12 [Homo sapiens]	0.75	0.96	0.90	1.66	0.68
PREDICTED: plectin isoform X13 [Homo sapiens]	0.95	0.96	1.43	1.64	0.96
PREDICTED: dynamin-1 isoform X13 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
PREDICTED: dynamin-1 isoform X14 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
PREDICTED: dynamin-1 isoform X15 [Homo sapiens]	0.46	0.38	0.25	0.31	0.35
PREDICTED: fructose-1,6-bisphosphatase 1 isoform X1 [Homo sapiens]	1.71	2.08	1.96	0.71	1.20
PREDICTED: ficolin-2 isoform X1 [Homo sapiens]	0.45	1.18	0.93	0.49	1.45
PREDICTED: formin-binding protein 1 isoform X21 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: formin-binding protein 1 isoform X22 [Homo sapiens]	2.58	1.00	1.50	2.16	1.51
PREDICTED: FK506-binding protein 15 isoform X1 [Homo sapiens]	1.64	1.21	0.94	0.98	1.54
PREDICTED: FK506-binding protein 15 isoform X2 [Homo sapiens]	1.64	1.21	0.94	0.98	1.54
PREDICTED: osteoclast-stimulating factor 1 isoform X1 [Homo sapiens]	1.00	0.80	2.16	1.39	1.48
PREDICTED: osteoclast-stimulating factor 1 isoform X2 [Homo sapiens]	1.00	0.80	2.16	1.39	1.48
PREDICTED: osteoclast-stimulating factor 1 isoform X3 [Homo sapiens]	1.00	0.80	2.16	1.39	1.48
PREDICTED: dipeptidyl peptidase 2 isoform X2 [Homo sapiens]	0.91	1.59	0.98	0.65	1.23

PREDICTED: tenascin isoform X5 [Homo sapiens]	1.54	4.13	0.95	0.61	1.42
PREDICTED: tenascin isoform X6 [Homo sapiens]	1.54	4.13	0.95	0.61	1.42
PREDICTED: tenascin isoform X7 [Homo sapiens]	1.54	4.13	0.95	0.61	1.42
PREDICTED: tenascin isoform X8 [Homo sapiens]	1.54	4.13	0.95	0.61	1.42
PREDICTED: tenascin isoform X9 [Homo sapiens]	1.34	4.33	0.98	0.62	1.94
PREDICTED: tenascin isoform X10 [Homo sapiens]	1.18	4.77	0.95	0.61	2.01
PREDICTED: nicotinamide riboside kinase 1 isoform X1 [Homo sapiens]	4.50	1.51	0.77	0.82	0.88
PREDICTED: nicotinamide riboside kinase 1 isoform X3 [Homo sapiens]	4.50	1.51	0.77	0.82	0.88
PREDICTED: nicotinamide riboside kinase 1 isoform X4 [Homo sapiens]	4.50	1.51	0.77	0.82	0.88
PREDICTED: serine/threonine-protein phosphatase 6 catalytic subunit isoform X1 [Homo sapiens]	2.08	1.40	0.84	1.52	0.80
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X1 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X3 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X4 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X5 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X6 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X7 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X8 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X9 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X10 [Homo sapiens]	0.80	2.32	1.18	2.59	1.48
PREDICTED: thioredoxin isoform X1 [Homo sapiens]	3.21	0.99	2.16	1.35	1.34
PREDICTED: nuclear pore complex protein Nup214 isoform X5 [Homo sapiens]	0.43	2.45	1.57	2.59	1.37
PREDICTED: polypyrimidine tract-binding protein 3 isoform X2 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
PREDICTED: polypyrimidine tract-binding protein 3 isoform X3 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
PREDICTED: polypyrimidine tract-binding protein 3 isoform X4 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
PREDICTED: polypyrimidine tract-binding protein 3 isoform X5 [Homo sapiens]	0.64	1.51	1.86	2.61	1.59
PREDICTED: abl interactor 1 isoform X4 [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
PREDICTED: abl interactor 1 isoform X5 [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
PREDICTED: abl interactor 1 isoform X6 [Homo sapiens]	1.41	0.74	0.58	0.51	0.94
PREDICTED: CUGBP Elav-like family member 2 isoform X14 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X16 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X17 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X18 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: CUGBP Elav-like family member 2 isoform X19 [Homo sapiens]	1.64	0.91	0.74	1.35	2.39
PREDICTED: phosphoribosyltransferase domain-containing protein 1 isoform X3 [Homo sapiens]	10.14	1.28	1.62	1.42	1.88
PREDICTED: phosphoribosyltransferase domain-	10.14	1.28	1.62	1.42	1.88

containing protein 1 isoform X4 [Homo sapiens]

PREDICTED: vimentin isoform X1 [Homo sapiens]	0.77	0.66	0.43	0.56	0.50
PREDICTED: cytosolic purine 5'-nucleotidase isoform X18 [Homo sapiens]	0.69	0.79	0.66	0.95	0.81
PREDICTED: AP-3 complex subunit mu-1 isoform X1 [Homo sapiens]	0.64	1.44	1.18	2.00	1.48
PREDICTED: heterogeneous nuclear ribonucleoprotein H3 isoform X8 [Homo sapiens]	0.91	0.85	0.84	1.39	0.84
PREDICTED: mannose-binding protein C isoform X1 [Homo sapiens]	0.64	2.08	1.00	0.79	1.22
PREDICTED: mannose-binding protein C isoform X4 [Homo sapiens]	0.64	2.08	1.00	0.79	1.22
PREDICTED: exocyst complex component 6 isoform X6 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X9 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X10 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: exocyst complex component 6 isoform X11 [Homo sapiens]	0.13	0.85	0.78	1.75	0.88
PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform isoform X5 [Homo sapiens]	0.88	1.00	1.30	1.80	1.00
PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform isoform X6 [Homo sapiens]	1.34	1.00	1.98	2.46	1.39
PREDICTED: phospholysine phosphohistidine inorganic pyrophosphate phosphatase isoform X4 [Homo sapiens]	1.00	0.70	0.40	0.24	0.50
PREDICTED: xaa-Pro aminopeptidase 1 isoform X3 [Homo sapiens]	1.31	0.95	2.69	1.81	2.30
PREDICTED: xaa-Pro aminopeptidase 1 isoform X4 [Homo sapiens]	1.00	0.91	1.18	1.65	0.93
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X12 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X13 [Homo sapiens]	0.33	0.65	0.84	1.74	0.68
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X14 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X15 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X16 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X17 [Homo sapiens]	0.77	1.40	1.41	2.15	1.17
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X18 [Homo sapiens]	2.02	1.70	2.33	3.88	2.01
PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X19 [Homo sapiens]	2.02	1.70	2.33	3.88	2.01
PREDICTED: lymphocyte-specific protein 1 isoform X5 [Homo sapiens]	0.28	0.81	0.64	0.91	0.88
PREDICTED: cysteine--tRNA ligase, cytoplasmic isoform X2 [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
PREDICTED: apoptosis inhibitor 5 isoform X1 [Homo sapiens]	0.50	0.85	0.70	0.69	0.79
PREDICTED: CD44 antigen isoform X11 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: CD44 antigen isoform X12 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37

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PREDICTED: CD44 antigen isoform X13 [Homo sapiens]	0.50	4.03	1.24	0.98	1.37
PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) isoform X4 [Homo sapiens]	1.31	2.08	1.00	0.77	1.82
PREDICTED: coiled-coil domain-containing protein 88B isoform X1 [Homo sapiens]	0.33	1.90	1.68	1.66	0.76
PREDICTED: coiled-coil domain-containing protein 88B isoform X2 [Homo sapiens]	0.33	1.90	1.68	1.66	0.76
PREDICTED: serine/threonine-protein kinase PAK 1 isoform X3 [Homo sapiens]	0.39	0.76	0.39	0.24	0.68
PREDICTED: serine/threonine-protein kinase PAK 1 isoform X5 [Homo sapiens]	0.39	0.76	0.39	0.24	0.68
PREDICTED: spectrin beta chain, non-erythrocytic 2 isoform X3 [Homo sapiens]	3.26	1.40	2.19	2.76	1.17
PREDICTED: spectrin beta chain, non-erythrocytic 2 isoform X4 [Homo sapiens]	3.26	1.40	2.19	2.76	1.17
PREDICTED: syntaxin-3 isoform X7 [Homo sapiens]	1.68	1.26	1.18	1.58	1.68
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X8 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X9 [Homo sapiens]	8.36	0.66	0.68	0.35	0.62
PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X10 [Homo sapiens]	4.40	0.58	0.74	0.31	0.60
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X20 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X21 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X22 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X23 [Homo sapiens]	0.88	1.25	0.92	0.78	1.21
PREDICTED: fermitin family homolog 3 isoform X1 [Homo sapiens]	1.54	0.84	1.72	1.56	1.23
PREDICTED: fermitin family homolog 3 isoform X2 [Homo sapiens]	2.49	0.92	1.27	1.60	1.82
PREDICTED: fermitin family homolog 3 isoform X3 [Homo sapiens]	1.47	0.93	1.34	2.18	2.68
PREDICTED: acetyl-CoA acetyltransferase, mitochondrial isoform X2 [Homo sapiens]	0.75	0.82	1.80	0.88	1.48
PREDICTED: cell surface glycoprotein MUC18 isoform X3 [Homo sapiens]	0.28	1.18	0.35	0.20	0.53
PREDICTED: cell surface glycoprotein MUC18 isoform X4 [Homo sapiens]	0.28	1.18	0.35	0.20	0.53
PREDICTED: cell surface glycoprotein MUC18 isoform X5 [Homo sapiens]	0.28	1.18	0.35	0.20	0.53
PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	1.41	1.88	1.69	1.65	1.56
PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X2 [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X3 [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X4 [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X5 [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform isoform X6 [Homo sapiens]	2.31	0.94	1.23	1.34	0.98
PREDICTED: fructose-2,6-bisphosphatase TIGAR isoform X1 [Homo sapiens]	2.54	1.96	1.74	1.60	1.26

PREDICTED: tyrosine-protein phosphatase non-receptor type 6 isoform X1 [Homo sapiens]	0.50	0.81	1.20	1.88	2.01
PREDICTED: alpha-2-macroglobulin isoform X1 [Homo sapiens]	0.33	0.85	0.39	0.20	0.65
PREDICTED: L-lactate dehydrogenase B chain isoform X1 [Homo sapiens]	5.72	1.53	2.31	1.97	2.30
PREDICTED: complement C1r subcomponent-like protein isoform X4 [Homo sapiens]	0.14	0.84	0.37	0.08	0.20
PREDICTED: complement C1r subcomponent-like protein isoform X5 [Homo sapiens]	0.14	0.84	0.37	0.08	0.20
PREDICTED: prostaglandin E synthase 3 isoform X8 [Homo sapiens]	2.50	1.96	1.61	2.30	1.39
PREDICTED: decorin isoform X2 [Homo sapiens]	24.68	0.75	0.71	0.57	0.83
PREDICTED: eukaryotic translation initiation factor 4B isoform X2 [Homo sapiens]	3.43	0.30	0.89	0.95	0.76
PREDICTED: keratin, type II cytoskeletal 3 isoform X2 [Homo sapiens]	0.88	2.08	1.87	0.66	3.64
PREDICTED: keratin, type II cytoskeletal 3 isoform X3 [Homo sapiens]	0.88	2.08	1.87	0.66	3.64
PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X3 [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X4 [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X5 [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X6 [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X9 [Homo sapiens]	3.70	1.45	2.01	1.28	2.01
PREDICTED: nucleosome assembly protein 1-like 1 isoform X15 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
PREDICTED: nucleosome assembly protein 1-like 1 isoform X16 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
PREDICTED: nucleosome assembly protein 1-like 1 isoform X17 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
PREDICTED: nucleosome assembly protein 1-like 1 isoform X18 [Homo sapiens]	6.69	1.56	1.95	2.10	1.21
PREDICTED: vacuolar protein sorting-associated protein 29 isoform X1 [Homo sapiens]	0.77	1.73	1.44	1.45	2.68
PREDICTED: vacuolar protein sorting-associated protein 29 isoform X4 [Homo sapiens]	0.77	1.73	1.44	1.45	2.68
PREDICTED: serine/threonine-protein phosphatase PP1-gamma catalytic subunit isoform X1 [Homo sapiens]	0.41	0.91	0.48	0.34	0.52
PREDICTED: 5'-AMP-activated protein kinase subunit gamma-1 isoform X4 [Homo sapiens]	4.74	0.95	2.26	2.53	2.34
PREDICTED: disco-interacting protein 2 homolog B isoform X2 [Homo sapiens]	0.21	1.35	0.66	0.78	1.26
PREDICTED: disco-interacting protein 2 homolog B isoform X3 [Homo sapiens]	0.21	1.35	0.66	0.78	1.26
PREDICTED: disco-interacting protein 2 homolog B isoform X4 [Homo sapiens]	0.21	1.35	0.66	0.78	1.26
PREDICTED: tyrosine-protein phosphatase non-receptor type 11 isoform X1 [Homo sapiens]	0.98	0.97	2.49	1.92	1.81
PREDICTED: tyrosine-protein phosphatase non-receptor type 11 isoform X2 [Homo sapiens]	0.98	0.97	2.49	1.92	1.81
PREDICTED: ras-related protein Rab-5B isoform X3 [Homo sapiens]	0.77	1.58	2.79	4.19	1.35
PREDICTED: rho GTPase-activating protein 9 isoform X2 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
PREDICTED: rho GTPase-activating protein 9 isoform X9 [Homo sapiens]	1.31	2.20	1.36	2.00	1.38
PREDICTED: ARF GTPase-activating protein GIT2 isoform X7 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X8 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39

PREDICTED: ARF GTPase-activating protein GIT2 isoform X9 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X10 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X11 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X12 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X13 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ARF GTPase-activating protein GIT2 isoform X14 [Homo sapiens]	1.18	0.92	1.79	3.37	1.39
PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X4 [Homo sapiens]	6.25	1.00	0.95	1.40	0.82
PREDICTED: heat shock protein 105 kDa isoform X3 [Homo sapiens]	1.24	0.79	1.51	0.67	0.56
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X13 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: rho guanine nucleotide exchange factor 7 isoform X14 [Homo sapiens]	1.21	0.87	0.49	0.26	0.87
PREDICTED: coagulation factor X isoform X2 [Homo sapiens]	0.88	0.61	0.21	0.11	0.27
PREDICTED: epididymal secretory protein E1 isoform X1 [Homo sapiens]	0.41	3.52	2.49	3.23	1.86
PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X1 [Homo sapiens]	0.88	2.20	1.56	4.33	1.63
PREDICTED: proteasome activator complex subunit 2 isoform X1 [Homo sapiens]	1.82	1.30	1.26	1.19	2.34
PREDICTED: proteasome activator complex subunit 2 isoform X2 [Homo sapiens]	1.82	1.30	1.26	1.19	2.34
PREDICTED: sorting nexin-6 isoform X1 [Homo sapiens]	1.18	2.32	1.00	0.87	0.92
PREDICTED: serine/threonine-protein kinase VRK1 isoform X3 [Homo sapiens]	0.54	0.77	0.68	0.99	0.88
PREDICTED: serine/threonine-protein kinase VRK1 isoform X2 [Homo sapiens]	0.54	0.77	0.68	0.99	0.88
PREDICTED: tryptophan--tRNA ligase, cytoplasmic isoform X5 [Homo sapiens]	1.68	0.93	2.09	2.83	1.17
PREDICTED: calmodulin isoform X1 [Homo sapiens]	1.57	1.65	1.88	1.70	2.20
PREDICTED: dmX-like protein 2 isoform X8 [Homo sapiens]	0.18	0.78	0.42	0.27	0.50
PREDICTED: tropomodulin-3 isoform X1 [Homo sapiens]	1.34	1.25	1.18	1.66	2.01
PREDICTED: ras-related protein Rab-8B isoform X1 [Homo sapiens]	0.62	0.64	0.56	0.49	0.78
PREDICTED: pyruvate kinase PKM isoform X4 [Homo sapiens]	0.88	0.95	1.60	1.69	1.27
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform X7 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform X8 [Homo sapiens]	22.56	0.93	1.43	0.98	2.76
PREDICTED: dual specificity mitogen-activated protein kinase kinase 1 isoform X3 [Homo sapiens]	2.19	0.77	2.29	1.34	1.88
PREDICTED: SAFB-like transcription modulator isoform X3 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: SAFB-like transcription modulator isoform X4 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: SAFB-like transcription modulator isoform X5 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: SAFB-like transcription modulator isoform X6 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: SAFB-like transcription modulator isoform X7 [Homo sapiens]		1.22	15.13	17.04	8.40
PREDICTED: AP-3 complex subunit beta-2 isoform X1 [Homo sapiens]	0.77	2.30	1.42	0.45	2.60
PREDICTED: AP-3 complex subunit beta-2 isoform X2	0.77	2.30	1.42	0.45	2.60

[Homo sapiens]

PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member A isoform X1

[Homo sapiens]	0.83	1.57	1.71	1.56	1.34
PREDICTED: talin-2 isoform X12 [Homo sapiens]	2.38	0.82	1.21	1.35	2.39
PREDICTED: talin-2 isoform X13 [Homo sapiens]	2.38	0.82	1.21	1.35	2.39
PREDICTED: talin-2 isoform X14 [Homo sapiens]	2.38	0.82	1.21	1.35	2.39
PREDICTED: talin-2 isoform X15 [Homo sapiens]	2.38	0.82	1.21	1.35	2.39
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X1 [Homo sapiens]	4.38	0.99	1.00	0.98	0.92
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X2 [Homo sapiens]	4.38	0.99	1.00	0.98	0.92
PREDICTED: GPI mannosyltransferase 3 isoform X3 [Homo sapiens]	1.64	0.92	1.83	3.33	2.30
PREDICTED: pyrin isoform X1 [Homo sapiens]	0.33	0.70	0.61	1.97	0.68
PREDICTED: putative RNA-binding protein Luc7-like 1 isoform X7 [Homo sapiens]	0.39	0.77	0.58	0.32	0.51
PREDICTED: transcription elongation factor B polypeptide 2 isoform X1 [Homo sapiens]	1.47	1.21	1.27	1.52	1.81
PREDICTED: SUMO-conjugating enzyme UBC9 isoform X3 [Homo sapiens]	1.64	2.59	1.41	1.31	1.23
PREDICTED: lipopolysaccharide-induced tumor necrosis factor-alpha factor isoform X3 [Homo sapiens]	2.38	1.17	2.00	2.51	1.44
PREDICTED: integrin alpha-M isoform X1 [Homo sapiens]	0.88	1.21	0.68	0.41	0.92
PREDICTED: sulfotransferase 1A2 isoform X1 [Homo sapiens]	0.28	0.83	0.68	0.83	2.53
PREDICTED: sulfotransferase 1A2 isoform X2 [Homo sapiens]	0.28	0.83	0.68	0.83	2.53
PREDICTED: sulfotransferase 1A1 isoform X2 [Homo sapiens]	0.45	0.73	0.61	0.85	2.53
PREDICTED: cholesteryl ester transfer protein isoform X1 [Homo sapiens]	0.25	0.53	0.40	0.23	0.77
PREDICTED: alanine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	4.16	1.17	2.02	1.87	1.23
PREDICTED: copine-7 isoform X2 [Homo sapiens]	0.80	1.53	1.24	2.02	1.81
PREDICTED: haptoglobin-related protein isoform X1 [Homo sapiens]	0.77	1.42	0.83	0.44	1.20
PREDICTED: interferon regulatory factor 8 isoform X1 [Homo sapiens]	1.41	0.94	0.44	0.24	0.57
PREDICTED: hydrocephalus-inducing protein homolog isoform X1 [Homo sapiens]	0.39	2.08	0.38	0.19	0.54
PREDICTED: lysophosphatidylcholine acyltransferase 2 isoform X2 [Homo sapiens]	0.45	1.22	1.78	2.32	0.92
PREDICTED: polyamine-modulated factor 1-binding protein 1 isoform X4 [Homo sapiens]	1.57	1.45	1.37	2.24	1.58
PREDICTED: rap1 GTPase-activating protein 2 isoform X4 [Homo sapiens]	0.91	0.84	0.58	0.39	0.54
PREDICTED: E3 ubiquitin-protein ligase RNF167 isoform X10 [Homo sapiens]		0.91	2.21	2.35	1.48
PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform X1 [Homo sapiens]	0.31	0.65	0.75	0.39	0.62
PREDICTED: beta-arrestin-2 isoform X1 [Homo sapiens]	1.31	0.85	0.54	0.66	0.73
PREDICTED: glyoxalase domain-containing protein 4 isoform X1 [Homo sapiens]	3.65	0.93	1.29	1.63	0.94
PREDICTED: ankyrin repeat and FYVE domain-containing protein 1 isoform X2 [Homo sapiens]	1.31	1.51	1.72	1.21	1.28
PREDICTED: phosphoribosylformylglycinamide synthase isoform X1 [Homo sapiens]	7.25	1.22	1.18	1.26	0.79
PREDICTED: T-complex protein 1 subunit zeta-2 isoform X1 [Homo sapiens]	2.79	0.97	2.29	1.57	1.63

PREDICTED: T-complex protein 1 subunit zeta-2 isoform X2 [Homo sapiens]	2.79	0.97	2.29	1.57	1.63
PREDICTED: 2',3'-cyclic-nucleotide 3'-phosphodiesterase isoform X2 [Homo sapiens]	14.12	0.94	0.78	0.87	0.80
PREDICTED: collagen alpha-1(I) chain isoform X1 [Homo sapiens]	1.54	2.39	1.54	0.49	2.50
PREDICTED: collagen alpha-1(I) chain isoform X2 [Homo sapiens]	1.54	3.41	0.92	0.62	2.50
PREDICTED: collagen alpha-1(I) chain isoform X3 [Homo sapiens]	1.54	2.39	1.54	0.49	2.50
PREDICTED: protein unc-13 homolog D isoform X1 [Homo sapiens]	0.95	1.40	0.58	0.57	0.90
PREDICTED: protein unc-13 homolog D isoform X2 [Homo sapiens]	0.95	1.40	0.58	0.57	0.90
PREDICTED: hematological and neurological expressed 1 protein isoform X1 [Homo sapiens]	0.39	0.82	1.72	2.27	0.53
PREDICTED: cytokine receptor-like factor 3 isoform X1 [Homo sapiens]	0.52	0.69	0.55	0.44	0.61
PREDICTED: 26S protease regulatory subunit 8 isoform X1 [Homo sapiens]	7.36	0.85	0.62	0.62	0.58
PREDICTED: serine/arginine-rich splicing factor 1 isoform X1 [Homo sapiens]	0.69	1.24	0.66	0.29	0.82
PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens]	0.80	1.44	1.26	1.23	1.19
PREDICTED: actin, cytoplasmic 2 isoform X2 [Homo sapiens]	0.67	1.44	1.38	1.42	1.36
PREDICTED: formin-like protein 1 isoform X1 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X2 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X3 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X4 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X5 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X6 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X7 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X8 [Homo sapiens]	0.54	0.97	1.19	1.61	1.54
PREDICTED: formin-like protein 1 isoform X9 [Homo sapiens]	0.98	0.95	1.19	1.61	1.54
PREDICTED: puromycin-sensitive aminopeptidase isoform X1 [Homo sapiens]	1.21	0.80	0.90	1.59	0.82
PREDICTED: puromycin-sensitive aminopeptidase-like protein-like isoform X1 [Homo sapiens]	0.83	0.84	1.00	1.63	0.90
PREDICTED: coiled-coil domain-containing protein 57 isoform X4 [Homo sapiens]	2.58	0.70	2.07	2.51	2.60
PREDICTED: structural maintenance of chromosomes flexible hinge domain-containing protein 1 isoform X2 [Homo sapiens]	5.87	0.78	1.00	1.97	0.75
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X8 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X9 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X10 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X11 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X12 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X13 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X14 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70

PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X15 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X16 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: E3 ubiquitin-protein ligase NEDD4-like isoform X17 [Homo sapiens]	1.51	1.51	0.51	0.34	0.70
PREDICTED: serpin B8 isoform X1 [Homo sapiens]	1.79	0.77	1.36	1.35	0.93
PREDICTED: cytosolic non-specific dipeptidase isoform X3 [Homo sapiens]	1.31	0.89	0.75	0.49	0.89
PREDICTED: vacuolar protein sorting-associated protein 4B isoform X1 [Homo sapiens]	1.61	0.78	0.89	2.83	0.94
PREDICTED: ATP-dependent RNA helicase DDX39A isoform X1 [Homo sapiens]	1.57	1.25	1.27	0.94	0.99
PREDICTED: N-acetylmuramoyl-L-alanine amidase isoform X1 [Homo sapiens]	0.35	0.68	0.29	0.16	0.44
PREDICTED: minor histocompatibility protein HA-1 isoform X1 [Homo sapiens]	0.45	0.68	0.50	0.79	0.75
PREDICTED: interleukin enhancer-binding factor 3 isoform X3 [Homo sapiens]	0.69	1.25	1.82	1.59	2.76
PREDICTED: glucosidase 2 subunit beta isoform X1 [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
PREDICTED: glucosidase 2 subunit beta isoform X3 [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
PREDICTED: glucosidase 2 subunit beta isoform X4 [Homo sapiens]	0.31	1.37	1.39	1.28	2.60
PREDICTED: dual specificity mitogen-activated protein kinase kinase 2 isoform X1 [Homo sapiens]	1.24	0.77	0.75	1.00	2.08
PREDICTED: scaffold attachment factor B1 isoform X1 [Homo sapiens]	0.52	1.25	3.48	7.80	1.40
PREDICTED: syntaxin-binding protein 2 isoform X1 [Homo sapiens]	1.44	0.98	1.58	2.21	1.28
PREDICTED: tropomyosin alpha-4 chain isoform X2 [Homo sapiens]	3.52	0.71	1.22	0.80	0.88
PREDICTED: AP-3 complex subunit delta-1 isoform X1 [Homo sapiens]	0.98	2.09	2.18	3.20	1.73
PREDICTED: splicing factor U2AF 65 kDa subunit isoform X1 [Homo sapiens]	1.71	1.40	2.56	1.89	1.20
PREDICTED: tubulin-folding cofactor B isoform X1 [Homo sapiens]	2.02	0.94	1.54	2.35	1.17
PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 1 isoform X3 [Homo sapiens]	1.34	3.43	3.39	5.65	1.80
PREDICTED: echinoderm microtubule-associated protein-like 2 isoform X1 [Homo sapiens]	0.56	1.34	0.69	0.69	1.23
PREDICTED: echinoderm microtubule-associated protein-like 2 isoform X2 [Homo sapiens]	0.56	1.34	0.69	0.69	1.23
PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]	1.47	0.94	0.75	0.56	1.23
PREDICTED: myosin-14 isoform X1 [Homo sapiens]	0.95	1.96	1.65	1.97	1.70
PREDICTED: alpha-actinin-4 isoform X3 [Homo sapiens]	0.77	2.08	1.46	1.66	1.23
PREDICTED: alpha-soluble NSF attachment protein isoform X1 [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
PREDICTED: alpha-soluble NSF attachment protein isoform X2 [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
PREDICTED: alpha-soluble NSF attachment protein isoform X3 [Homo sapiens]	1.89	0.94	0.90	1.21	1.90
PREDICTED: rho guanine nucleotide exchange factor 1 isoform X6 [Homo sapiens]	0.69	2.08	1.18	2.81	2.30
PREDICTED: signal-regulatory protein beta-1 isoform X6 [Homo sapiens]	0.50	1.56	1.21	0.94	1.52
PREDICTED: tyrosine-protein phosphatase non-receptor type substrate 1 isoform X3 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: tyrosine-protein phosphatase non-receptor type substrate 1 isoform X4 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98
PREDICTED: tyrosine-protein phosphatase non-receptor type substrate 1 isoform X5 [Homo sapiens]	0.57	1.95	1.71	1.57	1.98

PREDICTED: NSFL1 cofactor p47 isoform X1 [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
PREDICTED: NSFL1 cofactor p47 isoform X2 [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
PREDICTED: NSFL1 cofactor p47 isoform X4 [Homo sapiens]	3.08	0.89	0.75	0.44	0.88
PREDICTED: ral GTPase-activating protein subunit alpha-2 isoform X2 [Homo sapiens]	149.10	0.78	1.21	0.31	1.24
PREDICTED: ral GTPase-activating protein subunit alpha-2 isoform X3 [Homo sapiens]	149.10	0.78	1.21	0.31	1.24
PREDICTED: adenosine deaminase isoform X5 [Homo sapiens]	1.79	2.45	1.36	1.73	1.36
PREDICTED: RNA-binding protein Raly isoform X4 [Homo sapiens]	0.54	0.94	0.98	0.98	0.90
PREDICTED: RNA-binding protein Raly isoform X7 [Homo sapiens]	0.54	0.94	0.98	0.98	0.90
PREDICTED: engulfment and cell motility protein 2 isoform X9 [Homo sapiens]	0.14	0.57	1.21	1.70	0.74
PREDICTED: serine/threonine-protein kinase 4 isoform X5 [Homo sapiens]	0.64	0.66	0.57	0.87	0.66
PREDICTED: ES1 protein homolog, mitochondrial-like isoform X3 [Homo sapiens]	0.46	0.81	0.94	0.42	0.76
PREDICTED: histone H2B type F-S-like [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
PREDICTED: collagen alpha-1(VI) chain isoform X1 [Homo sapiens]	3.12	1.87	0.71	0.55	1.34
PREDICTED: integrin beta-2 isoform X1 [Homo sapiens]	0.56	0.92	0.79	0.31	0.96
PREDICTED: 6-phosphofructokinase, liver type isoform X5 [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
PREDICTED: 6-phosphofructokinase, liver type isoform X6 [Homo sapiens]	3.21	0.92	0.96	1.26	0.99
PREDICTED: bcl-2-like protein 13 isoform X1 [Homo sapiens]	0.83	0.81	0.50	0.46	0.62
PREDICTED: adenosine deaminase CECR1 isoform X1 [Homo sapiens]	0.80	0.97	0.99	0.79	0.73
PREDICTED: nuclear pore complex protein Nup50 isoform X5 [Homo sapiens]	0.39	0.94	1.00	1.42	0.96
PREDICTED: protein kinase C and casein kinase substrate in neurons protein 2 isoform X5 [Homo sapiens]	1.00	0.79	0.88	1.27	0.96
PREDICTED: beta-adrenergic receptor kinase 2 isoform X1 [Homo sapiens]	0.33	1.37	3.35	8.99	2.08
PREDICTED: RNA-binding protein EWS isoform X3 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
PREDICTED: RNA-binding protein EWS isoform X4 [Homo sapiens]	0.45	0.94	0.40	0.45	0.52
PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X2 [Homo sapiens]	9.20	0.73	0.64	0.66	0.74
PREDICTED: neurofilament heavy polypeptide isoform X2 [Homo sapiens]	0.77	0.58	0.53	1.98	0.44
PREDICTED: ras-related C3 botulinum toxin substrate 2 isoform X1 [Homo sapiens]	0.66	0.80	1.31	2.25	2.34
PREDICTED: apolipoprotein L3 isoform X3 [Homo sapiens]	0.56	0.67	0.31	0.19	0.53
PREDICTED: clathrin heavy chain 2 isoform X5 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: clathrin heavy chain 2 isoform X6 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: clathrin heavy chain 2 isoform X7 [Homo sapiens]	2.02	0.87	2.29	1.95	0.78
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X6 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X7 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73
PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X8 [Homo sapiens]	0.66	0.48	0.58	0.95	0.73

PREDICTED: serine/threonine-protein kinase PAK 3 isoform X7 [Homo sapiens]	0.98	0.58	0.71	0.57	0.70
PREDICTED: thyroxine-binding globulin isoform X2 [Homo sapiens]	0.46	1.51	0.46	0.28	0.68
PREDICTED: coagulation factor IX isoform X3 [Homo sapiens]	0.35	0.50	0.29	0.14	0.31
PREDICTED: septin-6 isoform X2 [Homo sapiens]	1.44	0.94	1.39	1.54	1.74
PREDICTED: SAM and SH3 domain-containing protein 3 isoform X1 [Homo sapiens]	1.37	0.63	0.50	0.50	0.63
PREDICTED: cullin-4B isoform X2 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
PREDICTED: cullin-4B isoform X3 [Homo sapiens]	0.67	0.91	1.24	1.25	0.83
PREDICTED: rho guanine nucleotide exchange factor 6 isoform X6 [Homo sapiens]	1.21	0.87	0.55	0.77	0.87
PREDICTED: prefoldin subunit 3 isoform X1 [Homo sapiens]	2.00	1.25	1.21	0.92	0.92
PREDICTED: ATP-dependent RNA helicase DDX3Y isoform X2 [Homo sapiens]	0.75	0.93	0.99	1.71	2.76
PREDICTED: ATP-dependent RNA helicase DDX3Y isoform X3 [Homo sapiens]	0.83	2.71	1.96	1.62	1.43
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	0.50	0.66	0.29	0.15	0.90
PREDICTED: heterogeneous nuclear ribonucleoprotein C-like 1-like [Homo sapiens]	0.98	2.45	1.63	3.87	1.62
PREDICTED: trypsin-2 isoform X4 [Homo sapiens]	1.61	0.48	0.20	0.13	0.32
PREDICTED: elongation factor 1-delta isoform X3 [Homo sapiens]	3.61	0.87	0.98	0.90	2.68
PREDICTED: elongation factor 1-delta isoform X4 [Homo sapiens]	0.25	0.83	0.71	0.44	0.67
PREDICTED: elongation factor 1-delta isoform X5 [Homo sapiens]	0.25	0.83	0.71	0.44	0.67
PREDICTED: cysteine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	3.86	0.96	1.56	1.53	0.91
PREDICTED: protein Z-dependent protease inhibitor isoform X1 [Homo sapiens]	0.66	0.98	0.65	0.32	0.70
PREDICTED: alpha-2-antiplasmin isoform X1 [Homo sapiens]	0.52	0.85	0.51	0.28	0.68
PREDICTED: vesicle-fusing ATPase isoform X1 [Homo sapiens]	1.21	1.73	0.89	0.95	1.40
PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	3.79	2.59	2.01	2.07	1.17
PREDICTED: puromycin-sensitive aminopeptidase-like protein-like isoform X2 [Homo sapiens]	1.31	0.84	1.00	1.63	0.90
PREDICTED: D-dopachrome decarboxylase-like protein isoform X2 [Homo sapiens]	3.26	0.93	0.83	0.85	0.92
PREDICTED: D-dopachrome decarboxylase isoform X1 [Homo sapiens]	5.20	1.96	0.83	0.85	0.92
PREDICTED: V-set and immunoglobulin domain-containing protein 1-like [Homo sapiens]	0.46	0.77	0.41	0.25	0.84
PREDICTED: apolipoprotein M isoform X1 [Homo sapiens]	0.26	0.57	0.30	0.18	0.45
PREDICTED: HLA class I histocompatibility antigen, A-2 alpha chain isoform X1 [Homo sapiens]	0.83	0.96	0.67	0.34	0.80
PREDICTED: HLA class I histocompatibility antigen, A-2 alpha chain isoform X2 [Homo sapiens]	0.83	0.96	0.67	0.34	0.80
PREDICTED: protein CutA isoform X1 [Homo sapiens]	1.44	1.18	0.88	0.82	0.89
PREDICTED: septin-7-like isoform X2 [Homo sapiens]	1.28	0.87	1.63	1.30	1.81
PREDICTED: septin-7-like isoform X3 [Homo sapiens]	1.28	0.87	1.63	1.30	1.81
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	1.79	0.73	0.57	0.28	0.88
PREDICTED: uncharacterized protein LOC102725101 [Homo sapiens]	0.09	0.66	0.28	0.16	0.53
PREDICTED: puromycin-sensitive aminopeptidase-like	0.83	0.84	1.00	1.63	0.90

protein-like isoform X4 [Homo sapiens]					
PREDICTED: puromycin-sensitive aminopeptidase-like protein-like [Homo sapiens]	1.31	0.84	1.00	1.63	0.90
PREDICTED: histone H2B type F-S-like [Homo sapiens]	0.31	20.86	1.86	0.32	3.79
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X1 [Homo sapiens]	0.57	1.25	0.90	1.97	1.57
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X2 [Homo sapiens]	0.57	1.25	0.90	1.97	1.57
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X3 [Homo sapiens]	0.57	1.25	0.90	1.97	1.57
isocitrate dehydrogenase [NADP], mitochondrial isoform 2 [Homo sapiens]	1.34	1.62	2.01	1.68	1.25
serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform d [Homo sapiens]	0.77	0.82	0.62	0.55	0.68
putative alpha-1-antitrypsin-related protein precursor [Homo sapiens]	0.19	2.53	2.49	0.79	1.47
bridging integrator 2 isoform 4 [Homo sapiens]	0.50	0.84	0.51	0.43	0.58
coatamer subunit gamma-2 isoform 2 [Homo sapiens]	1.64	0.92	1.83	3.33	2.30
bridging integrator 2 isoform 1 [Homo sapiens]	0.80	0.96	0.80	0.63	1.94
bridging integrator 2 isoform 3 [Homo sapiens]	0.64	0.93	0.63	0.56	0.75
bridging integrator 2 isoform 2 [Homo sapiens]	0.80	0.96	0.80	0.63	1.94
general vesicular transport factor p115 isoform 2 [Homo sapiens]	3.17	1.26	0.48	0.46	0.57
general vesicular transport factor p115 isoform 1 [Homo sapiens]	0.66	0.93	0.67	0.70	0.74
isocitrate dehydrogenase [NADP], mitochondrial isoform 3 [Homo sapiens]	1.21	0.99	1.80	1.57	1.30
ribosyldihydronicotinamide dehydrogenase [quinone] isoform 2 [Homo sapiens]	2.38	2.45	1.46	1.77	1.30
dedicator of cytokinesis protein 10 DOCK10.2 [Homo sapiens]	0.26	2.19	1.34	0.54	1.61
eukaryotic translation initiation factor 4 gamma 1 isoform 7 [Homo sapiens]	2.66	1.51	1.21	2.17	0.89
polyubiquitin-C [Homo sapiens]	6.97	1.22	1.36	1.22	1.22
serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform isoform b [Homo sapiens]	1.34	1.00	1.98	2.46	1.39
heterogeneous nuclear ribonucleoprotein C-like [Homo sapiens]	0.98	2.45	1.63	3.87	1.62
peptidyl-prolyl cis-trans isomerase A-like 4A/B/C [Homo sapiens]	4.58	1.90	2.68	2.49	1.93
mesencephalic astrocyte-derived neurotrophic factor precursor [Homo sapiens]	0.39	1.28	1.52	1.29	1.76
cytoplasmic FMR1-interacting protein 2 isoform b [Homo sapiens]	2.17	0.96	0.93	2.32	1.33
cytoplasmic FMR1-interacting protein 2 isoform c [Homo sapiens]	2.17	0.96	0.93	2.32	1.33
basement membrane-specific heparan sulfate proteoglycan core protein isoform a precursor [Homo sapiens]	1.37	4.07	2.56	0.83	3.52
ras-related protein Rap-1A precursor [Homo sapiens]	0.98	1.36	1.69	1.80	1.45
SPARC-like protein 1 isoform 2 [Homo sapiens]	0.11	1.53	0.75	0.53	2.30
wiskott-Aldrich syndrome protein family member 3 isoform 2 [Homo sapiens]	0.80	0.85	2.76	0.42	1.22
carbonic anhydrase 1 isoform b [Homo sapiens]	100.17	0.91	2.29	0.29	1.21
carbonic anhydrase 1 isoform c [Homo sapiens]	80.01	0.91	1.26	0.29	1.61
eukaryotic peptide chain release factor subunit 1 isoform 2 [Homo sapiens]	1.93	1.30	1.64	1.82	1.27
carboxypeptidase N subunit 2 precursor [Homo sapiens]	2.38	1.18	0.66	0.35	0.61
beta-hexosaminidase subunit beta isoform 2 [Homo sapiens]	1.37	1.25	2.69	0.77	0.93

ras-related protein Rab-5A isoform 2 [Homo sapiens]	0.35	1.42	2.17	3.39	1.74
hematopoietic lineage cell-specific protein isoform 2 [Homo sapiens]	0.41	0.78	0.55	0.67	0.71
mitogen-activated protein kinase 4 isoform 3 [Homo sapiens]	2.11	1.96	2.07	2.33	2.05
beta-glucuronidase isoform 3 [Homo sapiens]	0.83	1.54	1.50	0.88	1.17
beta-glucuronidase isoform 4 [Homo sapiens]	0.83	1.54	1.50	0.88	1.17
major vault protein isoform 2 [Homo sapiens]	0.77	1.26	1.36	1.73	2.45
major vault protein isoform 3 [Homo sapiens]	0.77	1.21	1.34	1.71	2.45
tubulin beta chain isoform a [Homo sapiens]	1.21	0.76	1.60	0.71	0.84
tubulin beta chain isoform c [Homo sapiens]	1.00	0.75	1.27	0.60	0.89
tubulin beta chain isoform d [Homo sapiens]	1.21	0.76	0.95	0.82	0.80
tubulin beta chain isoform e [Homo sapiens]	1.21	0.76	0.95	0.82	0.80
aspartate--tRNA ligase, cytoplasmic isoform 2 [Homo sapiens]	2.66	2.08	1.80	2.30	1.56
carbonic anhydrase 2 isoform 2 [Homo sapiens]	58.09	0.79	0.87	0.27	0.92
septin-9 isoform g [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
septin-9 isoform h [Homo sapiens]	0.64	1.96	2.18	2.00	1.41
aldehyde dehydrogenase family 1 member A3 isoform 2 [Homo sapiens]	20.90	0.87	0.77	0.51	0.81
lupus La protein [Homo sapiens]	1.57	0.91	0.91	0.98	0.64
heterogeneous nuclear ribonucleoprotein M isoform c [Homo sapiens]	1.57	0.80	0.82	2.11	1.61
hepatocyte growth factor activator isoform 1 preproprotein [Homo sapiens]	1.21	0.63	0.37	0.23	0.54
heterogeneous nuclear ribonucleoprotein R isoform 5 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
heterogeneous nuclear ribonucleoprotein R isoform 7 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
heterogeneous nuclear ribonucleoprotein R isoform 6 [Homo sapiens]	0.50	1.71	1.29	2.09	1.69
(Bos taurus) 81 kDa protein	9.77	0.91	0.58	0.32	0.67
(Bos taurus) hypothetical protein	0.66	1.90	0.68	0.41	0.81
(Bos taurus) similar to peptidoglycan recognition protein L	0.33	0.54	0.27	0.19	0.50
(Bos taurus) 54 kDa protein	0.28	0.91	0.46	0.26	0.58
(Bos taurus) 55 kDa protein	0.64	2.37	0.81	0.68	1.81
(Bos taurus) 68 kDa protein	1.96	0.63	0.29	0.16	0.54
(Bos taurus) 55 kDa protein	0.66	0.73	0.34	0.15	0.50
(Bos taurus) 121 kDa protein		3.62	0.82	0.71	2.08
(Bos taurus) similar to apolipoprotein B, partial	0.33	0.46	0.31	0.28	0.28
(Bos taurus) 63 kDa protein	4.12	0.77	0.31	0.19	0.50
Tax_Id=9606 Gene_Symbol=- Similar to Keratin, type II cytoskeletal 8	2.46	1.47	4.75	1.21	3.15
SWISS-PROT:O95678 Tax_Id=9606 Gene_Symbol=KRT75 Keratin, type II cytoskeletal 75	1.34	2.59	0.88	0.69	1.48
SWISS-PROT:P00735 (Bos taurus) Prothrombin precursor (Fragment)	0.33	0.63	0.41	0.23	0.54
Trypsin - Sus scrofa (Pig).	1.76	0.53	0.22	0.14	0.35
SWISS-PROT:P01030 (Bos taurus) similar to Complement C4-A precursor	2.54	0.85	0.57	0.30	0.68
SWISS-PROT:P01966 (Bos taurus) Hemoglobin subunit alpha	19.54	0.85	0.49	0.35	0.75
SWISS-PROT:P02070 (Bos taurus) Hemoglobin subunit beta	102.06	0.94	0.77	0.20	0.91
SWISS-PROT:P02533 Tax_Id=9606 Gene_Symbol=KRT14 Keratin, type I cytoskeletal 14	0.77	0.73	1.00	0.49	1.24
SWISS-PROT:P02535-1 Tax_Id=10090 Gene_Symbol=Krt10 Isoform 1 of Keratin, type I	0.77	0.74	0.22	0.11	0.48

cytoskeletal 10

SWISS-PROT:P02538 Tax_Id=9606					
Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A	1.51	1.21	3.34	1.97	4.30
SWISS-PROT:P02584 (Bos taurus) Profilin-1	0.62	1.24	1.52	2.00	1.40
SWISS-PROT:P02672 (Bos taurus) Fibrinogen alpha chain precursor	3.34	3.93	3.12	3.21	11.78
SWISS-PROT:P02676 (Bos taurus) similar to Fibrinogen beta chain precursor	0.69	2.71	0.82	0.85	1.99
SWISS-PROT:P02768-1 Tax_Id=9606					
Gene_Symbol=ALB Isoform 1 of Serum albumin precursor	0.26	0.77	0.25	0.11	0.41
SWISS-PROT:P02769 (Bos taurus) Bovine serum albumin precursor	0.75	0.77	0.27	0.14	0.43
SWISS-PROT:P04258 (Bos taurus) Similar to Collagen alpha 1(III) chain	2.02	3.32	3.92	0.88	5.01
SWISS-PROT:P04259 Tax_Id=9606					
Gene_Symbol=KRT6B Keratin, type II cytoskeletal 6B	1.51	1.21	3.34	1.97	4.30
SWISS-PROT:P04264 Tax_Id=9606					
Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1	1.61	0.77	0.33	0.18	0.45
SWISS-PROT:P06868 (Bos taurus) Plasminogen precursor	0.23	0.58	0.39	0.20	0.71
SWISS-PROT:P07224 (Bos taurus) Vitamin K-dependent protein S precursor	0.67	2.59	0.64	0.43	0.92
SWISS-PROT:P07477 Tax_Id=9606					
Gene_Symbol=PRSS1 Trypsin-1 precursor	1.61	0.49	0.21	0.13	0.32
SWISS-PROT:P08727 Tax_Id=9606					
Gene_Symbol=KRT19 Keratin, type I cytoskeletal 19	0.77	0.80	0.93	0.57	1.87
SWISS-PROT:P08729 Tax_Id=9606					
Gene_Symbol=KRT7 Keratin, type II cytoskeletal 7	0.52	0.21	0.30	0.23	0.15
SWISS-PROT:P12035 Tax_Id=9606					
Gene_Symbol=KRT3 Keratin, type II cytoskeletal 3	0.88	2.08	1.87	0.66	3.64
SWISS-PROT:P12763 (Bos taurus) Alpha-2-HS-glycoprotein precursor	0.09	0.51	0.25	0.18	0.35
SWISS-PROT:P13645 Tax_Id=9606					
Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10	2.38	0.78	0.45	0.18	0.56
SWISS-PROT:P13647 Tax_Id=9606					
Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5	2.38	0.64	0.78	0.37	1.28
SWISS-PROT:P15497 (Bos taurus) Apolipoprotein A-I precursor	0.33	0.61	0.19	0.10	0.20
SWISS-PROT:P17690 (Bos taurus) Beta-2-glycoprotein 1 precursor	0.16	0.68	0.34	0.16	0.43
SWISS-PROT:P19001 Tax_Id=10090					
Gene_Symbol=Krt19 Keratin, type I cytoskeletal 19	1.64	2.59	1.22	0.71	1.88
SWISS-PROT:P21752 (Bos taurus) Thymosin beta-9	0.57	0.92	1.36	1.24	0.77
SWISS-PROT:P28800 (Bos taurus) Alpha-2-antiplasmin precursor	0.31	0.89	0.49	0.29	0.67
SWISS-PROT:P35527 Tax_Id=9606					
Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9	2.31	0.89	0.35	0.25	0.43
SWISS-PROT:P35908 Tax_Id=9606					
Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal	0.77	0.63	0.27	0.15	0.50
SWISS-PROT:P41361 (Bos taurus) Antithrombin-III precursor	0.28	0.76	0.31	0.16	0.56
SWISS-PROT:P50446 Tax_Id=10090					
Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A	1.28	1.21	2.26	0.95	3.34
SWISS-PROT:P50448 (Bos taurus) Factor XIIa inhibitor precursor	0.88	1.37	0.78	0.52	1.25
SWISS-PROT:Q03247 (Bos taurus) Apolipoprotein E precursor	0.39	0.85	0.43	0.29	0.40
SWISS-PROT:Q05443 (Bos taurus) Lumican precursor	3.70	2.08	0.29	0.11	0.22
TREMBL:Q01IK2 (Bos taurus) Transferrin	0.19	0.63	0.21	0.11	0.40
TREMBL:Q0V8M9;Q9TRI0 (Bos taurus) similar to inter-alpha (globulin) inhibitor H3 isoform 2	0.80	1.37	1.90	0.68	1.47
TREMBL:Q0VCM5 (Bos taurus) Similar to Inter-alpha-trypsin inhibitor heavy chain H1	0.50	0.94	0.39	0.19	0.46

TREMBL:Q148H6 (Bos taurus) Hypothetical protein MGC139876	0.80	0.91	0.18	0.12	0.40
TREMBL:Q1A7A4 (Bos taurus) similar to complement component C5	0.39	1.51	0.79	0.52	2.30
TREMBL:Q1RMN8 (Bos taurus) Similar to Immunoglobulin lambda-like polypeptide 1	0.16	0.79	0.29	0.15	0.55
SWISS-PROT:Q28065 (Bos taurus) C4b-binding protein alpha chain precursor	0.56	1.37	0.83	0.52	1.21
TREMBL:Q28194 (Bos taurus) Thrombospondin-1	4.16	2.46	0.81	0.41	1.42
SWISS-PROT:Q29443 Serotransferrin - Bos taurus (Bovine).	0.19	0.63	0.21	0.11	0.40
SWISS-PROT:Q29RQ1 (Bos taurus) Complement component C7 precursor	0.46	0.66	0.30	0.16	0.38
TREMBL:Q2HJF0 (Bos taurus) Similar to Serotransferrin	0.19	0.61	0.20	0.11	0.35
TREMBL:Q2KIG3 (Bos taurus) Similar to carboxypeptidase B2	1.00	0.43	0.31	0.15	0.38
SWISS-PROT:Q2KIS7 (Bos taurus) Tetranectin precursor	0.35	0.84	0.39	0.31	0.45
TREMBL:Q2KJC7;Q8HZM3 (Bos taurus) Periostin, osteoblast specific factor	1.64	0.78	0.66	0.22	1.18
TREMBL:Q2KJF1 (Bos taurus) Alpha-1-B glycoprotein	0.46	2.71	0.46	0.21	0.51
SWISS-PROT:Q2UVX4 (Bos taurus) Complement C3 precursor	2.00	0.84	0.45	0.29	0.73
TREMBL:Q32PI4 (Bos taurus) Similar to complement factor I	0.75	1.00	0.58	0.30	0.66
SWISS-PROT:Q32PJ2 (Bos taurus) Apolipoprotein A-IV precursor	0.10	0.30	0.14	0.05	0.13
TREMBL:Q3KNV1;Q96GE1 Tax_Id=9606 Gene_Symbol=KRT7 keratin 7	0.52	0.21	0.30	0.23	0.15
TREMBL:Q3KUS7 (Bos taurus) Complement factor B	1.34	1.19	0.71	0.32	0.87
SWISS-PROT:Q3MHN2 (Bos taurus) Complement component C9 precursor	0.75	1.89	2.09	0.53	1.82
SWISS-PROT:Q3MHN5 (Bos taurus) Vitamin D-binding protein precursor	0.28	0.91	0.46	0.26	0.58
TREMBL:Q3SX09 (Bos taurus) similar to HBG protein	53.82	0.85	1.26	0.41	1.00
TREMBL:Q3SX14 (Bos taurus) Similar to Gelsolin	0.54	0.94	0.75	0.44	0.57
TREMBL:Q3SX28;Q5KR48 (Bos taurus) Tropomyosin 2	4.74	0.73	0.84	0.57	0.68
TREMBL:Q3SZV7 (Bos taurus) Similar to hemopexin	0.19	0.88	0.37	0.25	0.71
SWISS-PROT:Q3TTY5 Tax_Id=10090 Gene_Symbol=Krt2 Keratin, type II cytoskeletal 2 epidermal	1.24	0.71	0.28	0.14	0.58
SWISS-PROT:Q3ZBD7 (Bos taurus) Glucose-6-phosphate isomerase	0.75	1.21	1.43	1.18	1.24
TREMBL:Q3ZBS7 (Bos taurus) Vitronectin	0.75	0.54	0.49	0.24	0.80
SWISS-PROT:Q5XQN5 (Bos taurus) Keratin, type II cytoskeletal 5	1.34	0.63	0.32	0.16	0.43
SWISS-PROT:Q6IFX2 Tax_Id=10090 Gene_Symbol=Krt42 Keratin, type I cytoskeletal 42	0.77	0.76	2.19	0.85	3.69
TREMBL:Q6IME9 Tax_Id=10090 Gene_Symbol=Krt72 Type-II keratin Kb35	0.45	0.66	0.29	0.16	0.42
SWISS-PROT:Q7Z3Y7 Tax_Id=9606 Gene_Symbol=KRT28 Keratin 25D	0.80	0.91	0.18	0.12	0.40
SWISS-PROT:Q7Z3Y8 Tax_Id=9606 Gene_Symbol=KRT27 Keratin, type I cytoskeletal 27	0.80	0.91	0.18	0.12	0.40
TREMBL:Q8BGZ7;Q99MH7 Tax_Id=10090 Gene_Symbol=Krt75 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732475I03 product:CYTOKERATIN homolog	1.47	1.40	0.77	0.46	0.96
TREMBL:Q8VED5 Tax_Id=10090 Gene_Symbol=Krt79 Keratin 79	1.34	2.59	0.88	0.69	1.48
SWISS-PROT:Q922U2 Tax_Id=10090 Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5	1.34	0.63	0.32	0.16	0.43

SWISS-PROT:Q95121 (Bos taurus) Pigment epithelium-derived factor precursor	10.34	3.59	1.21	1.47	2.46
SWISS-PROT:Q9DCV7 Tax_Id=10090					
Gene_Symbol=Krt7 Keratin, type II cytoskeletal 7	0.52	0.21	0.30	0.23	0.15
TREMBL:Q9H552 Tax_Id=9606 Gene_Symbol=-					
Keratin-8-like protein 1	0.52	0.21	0.30	0.23	0.15
SWISS-PROT:Q9QWL7 Tax_Id=10090					
Gene_Symbol=Krt17 Keratin, type I cytoskeletal 17	0.77	0.89	0.93	0.59	1.23
TREMBL:Q9TR11 (Bos taurus) similar to inter-alpha-trypsin inhibitor heavy chain2	0.39	0.52	0.25	0.14	0.42
SWISS-PROT:Q9TT36 (Bos taurus) Thyroxine-binding globulin precursor	0.56	2.08	0.42	0.24	0.60
(Bos taurus) similar to afamin	0.21	0.66	0.24	0.12	0.50

APPENDIX B. iTRAQ 4 PLEX

Description	Ratios: F1: (Channel2, Sample) / (Channel1, Control)	Ratios: F1: (Channel3, Sample) / (Channel1, Control)	Ratios: F1: (Channel4, Sample) / (Channel1, Control)	Ratios of Serum+/Serum-
alcohol dehydrogenase 1A [Homo sapiens]	0.93	2.03	0.69	0.34
alcohol dehydrogenase 1C [Homo sapiens]	0.93	2.03	0.69	0.34
afamin precursor [Homo sapiens]	0.84	3.65	3.46	0.95
adenylate kinase isoenzyme 1 [Homo sapiens]	4.25	0.29	0.27	0.91
protein AMBP preproprotein [Homo sapiens]	2.24	8.71	7.99	0.92
pancreatic alpha-amylase precursor [Homo sapiens]	2.07	1.79	1.94	1.09
amyloid beta A4 precursor protein-binding family B member 1 isoform a [Homo sapiens]	2.49	43.95	58.97	1.34
serum amyloid P-component precursor [Homo sapiens]	1.00	6.26	6.04	0.96
amyloid-like protein 2 isoform 1 precursor [Homo sapiens]	2.49	9.52	5.88	0.62
apolipoprotein A-II preproprotein [Homo sapiens]	0.43	0.21	0.11	0.64
apolipoprotein C-I precursor [Homo sapiens]	0.74	0.59	0.63	0.99
apolipoprotein C-IV precursor [Homo sapiens]	0.95	4.44	1.76	0.40
antithrombin-III precursor [Homo sapiens]	2.07	6.25	5.85	0.94
zinc-alpha-2-glycoprotein precursor [Homo sapiens]	1.21	8.74	8.88	1.02

flavin reductase (NADPH) [Homo sapiens]	0.76	0.21	0.16	0.80
complement component C9 precursor [Homo sapiens]	2.24	6.20	7.75	1.25
calpain small subunit 1 [Homo sapiens]	2.07	0.26	0.24	0.91
chitotriosidase-1 isoform 1 precursor [Homo sapiens]	3.57	1.58	1.76	1.11
D-dopachrome decarboxylase [Homo sapiens]	0.99	0.22	0.10	0.46
elongation factor 1-alpha 1 [Homo sapiens]	0.76	0.08	0.05	0.75
elongation factor 1-alpha 2 [Homo sapiens]	0.79	0.08	0.05	0.73
elongation factor 2 [Homo sapiens]	0.58	0.35	0.31	0.88
alpha-enolase isoform 1 [Homo sapiens]	1.43	0.10	0.08	0.83
eosinophil peroxidase preproprotein [Homo sapiens]	3.44	0.35	0.16	0.47
coagulation factor IX preproprotein [Homo sapiens]	2.60	7.87	7.63	0.97
fibrinogen alpha chain isoform alpha-E preproprotein [Homo sapiens]	1.34	0.14	0.14	0.95
peptidyl-prolyl cis-trans isomerase FKBP4 [Homo sapiens]	0.89	0.21	0.49	2.31
protein flightless-1 homolog isoform 1 [Homo sapiens]	2.30	0.27	0.22	0.80
rab GDP dissociation inhibitor alpha [Homo sapiens]	0.97	0.22	0.20	0.90
glial fibrillary acidic protein isoform 1 [Homo sapiens]	2.07	0.13	0.07	0.56
gelsolin isoform a precursor [Homo sapiens]	2.60	6.89	6.78	0.98
glutathione S-transferase P [Homo sapiens]	0.81	0.19	0.15	0.89
histone H2A type 1-C [Homo sapiens]	3.93	0.91	0.37	0.40
histone H2A type 1 [Homo sapiens]	3.93	0.91	0.37	0.40
histone H2AX [Homo sapiens]	3.89	0.91	0.37	0.40
histone H2A.Z [Homo sapiens]	4.00	0.13	0.09	0.66
histone H2B type 1-L [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2B type 1-N [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2B type 1-M [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2B type 1-H [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2B type 2-E [Homo sapiens]	3.33	0.13	0.07	0.51

histone H3.1 [Homo sapiens]	4.78	0.07	0.04	0.57
histone H3.1t [Homo sapiens]	4.78	0.07	0.04	0.57
histone H4 [Homo sapiens]	3.10	0.10	0.08	0.75
hemoglobin subunit alpha [Homo sapiens]	0.58	0.05	0.75	5.80
hemoglobin subunit beta [Homo sapiens]	0.55	0.05	0.93	6.70
heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2 [Homo sapiens]	0.76	0.07	0.65	4.25
histidine-rich glycoprotein precursor [Homo sapiens]	1.58	7.29	6.21	0.85
10 kDa heat shock protein, mitochondrial [Homo sapiens]	1.43	0.27	0.13	0.47
interleukin-18 isoform 1 proprotein [Homo sapiens]	0.97	0.10	0.08	0.77
neutrophil collagenase preproprotein [Homo sapiens]	2.16	0.17	0.14	0.83
ran-specific GTPase-activating protein isoform 2 [Homo sapiens]	1.00	0.56	0.14	0.26
retinoic acid receptor responder protein 2 precursor [Homo sapiens]	2.60	3.51	2.74	0.78
radixin isoform 2 [Homo sapiens]	1.21	0.20	0.14	0.74
non-secretory ribonuclease precursor [Homo sapiens]	1.87	1.19	1.00	0.84
dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Homo sapiens]	0.42	0.04	0.04	0.96
protein S100-A4 [Homo sapiens]	1.18	0.13	0.07	0.57
protein S100-A9 [Homo sapiens]	3.66	0.22	0.12	0.54
ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	0.79	0.05	0.05	1.25
SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	2.60	0.30	0.24	0.81
alpha-synuclein isoform NACP140 [Homo sapiens]	0.48	0.08	0.07	0.89
small nuclear ribonucleoprotein F [Homo sapiens]	0.99	0.56	0.70	1.25
superoxide dismutase [Cu-Zn] [Homo sapiens]	0.95	0.18	0.19	1.08
SPARC precursor [Homo sapiens]	0.92	2.49	2.19	0.88
signal recognition particle 9 kDa protein isoform 2 [Homo sapiens]	1.19	0.04	0.92	20.71
transforming growth factor-beta-induced protein ig-h3 precursor [Homo sapiens]	2.07	3.65	2.80	0.77
ubiquitin-conjugating enzyme E2 N	0.88	0.85	0.32	0.38

[Homo sapiens]				
ubiquitin-conjugating enzyme E2 variant 2 [Homo sapiens]	0.84	0.10	0.13	1.33
vasodilator-stimulated phosphoprotein [Homo sapiens]	1.61	0.08	0.04	0.51
vascular cell adhesion protein 1 isoform a precursor [Homo sapiens]	2.07	4.76	7.84	1.65
vinculin isoform VCL [Homo sapiens]	1.21	0.49	0.48	0.99
14-3-3 protein beta/alpha [Homo sapiens]	0.89	1.34	0.91	0.68
14-3-3 protein eta [Homo sapiens]	0.88	0.16	0.35	2.20
complement component C8 alpha chain precursor [Homo sapiens]	2.07	6.83	7.76	1.14
fatty acid-binding protein, epidermal [Homo sapiens]	0.57	0.08	0.81	4.45
fumarylacetoacetase [Homo sapiens]	0.84	1.67	1.34	0.80
glutamate--cysteine ligase catalytic subunit isoform a [Homo sapiens]	0.65	0.50	0.52	0.98
epididymal secretory glutathione peroxidase isoform 1 precursor [Homo sapiens]	1.76	18.04	23.27	1.29
mast/stem cell growth factor receptor Kit isoform 1 precursor [Homo sapiens]	1.41	2.82	2.00	0.71
keratin, type I cytoskeletal 17 [Homo sapiens]	0.60	0.10	0.07	0.75
mannose-binding protein C precursor [Homo sapiens]	1.27	8.08	5.18	0.64
myeloperoxidase precursor [Homo sapiens]	3.31	0.17	0.14	0.82
myocilin precursor [Homo sapiens]	1.69	1.47	1.25	0.85
nucleoside diphosphate kinase A isoform b [Homo sapiens]	0.95	0.18	0.13	0.74
serotransferrin precursor [Homo sapiens]	0.66	0.08	0.07	0.87
phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	1.90	5.58	6.36	1.14
lysozyme C precursor [Homo sapiens]	2.00	0.06	0.05	0.76
rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens]	1.90	0.22	0.12	0.54
beta-2-microglobulin precursor [Homo sapiens]	0.99	4.36	5.05	1.16
calreticulin precursor [Homo sapiens]	2.60	2.49	0.83	0.33
cadherin-1 preproprotein [Homo sapiens]	0.78	1.88	1.79	0.92

calponin-2 isoform a [Homo sapiens]	0.71	0.17	0.15	0.87
di-N-acetylchitobiase precursor [Homo sapiens]	2.49	3.37	2.58	0.77
eukaryotic translation initiation factor 2 subunit 1 [Homo sapiens]	1.31	0.06	0.70	12.31
alpha-endosulfine isoform 3 [Homo sapiens]	1.19	0.07	0.09	1.20
protein disulfide-isomerase A4 precursor [Homo sapiens]	1.52	1.97	0.85	0.43
flap endonuclease 1 [Homo sapiens]	0.92	4.10	3.18	0.78
polypeptide N- acetylgalactosaminyltransferase 2 precursor [Homo sapiens]	1.74	2.59	2.76	1.06
glia maturation factor gamma [Homo sapiens]	0.99	0.13	0.13	0.96
glia maturation factor beta [Homo sapiens]	0.99	0.14	0.11	0.83
platelet glycoprotein V precursor [Homo sapiens]	1.43	6.85	7.35	1.07
glutathione S-transferase omega-1 isoform 1 [Homo sapiens]	1.37	0.47	0.48	1.03
hyaluronan-binding protein 2 isoform 1 preproprotein [Homo sapiens]	0.97	4.17	4.26	1.02
hepatoma-derived growth factor isoform a [Homo sapiens]	1.52	0.12	0.07	0.63
peroxiredoxin-6 [Homo sapiens]	2.79	0.10	0.10	0.98
peptidyl-prolyl cis-trans isomerase B precursor [Homo sapiens]	1.37	0.37	0.43	1.14
proteasome subunit beta type-8 isoform E1 proprotein [Homo sapiens]	0.89	0.26	0.27	1.02
serum deprivation-response protein [Homo sapiens]	5.79	11.51	16.09	1.40
osteopontin isoform OPN-b precursor [Homo sapiens]	2.60	2.15	2.00	0.93
tubulin-specific chaperone A isoform 2 [Homo sapiens]	0.76	0.42	0.40	0.92
annexin A3 [Homo sapiens]	2.49	0.26	0.15	0.57
F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	0.96	0.25	0.27	1.08
copper chaperone for superoxide dismutase [Homo sapiens]	0.96	0.47	0.54	1.16
desmocollin-1 isoform Dsc1b preproprotein [Homo sapiens]	2.49	4.21	3.19	0.76
haptoglobin isoform 1 preproprotein [Homo sapiens]	0.89	0.65	0.15	0.23
insulin-like growth factor-binding	0.97	4.18	4.53	1.08

protein complex acid labile subunit isoform 2 precursor [Homo sapiens]				
osteomodulin precursor [Homo sapiens]	2.46	2.98	3.89	1.30
profilin-1 [Homo sapiens]	0.88	0.13	0.12	0.99
serpin B10 [Homo sapiens]	3.19	0.34	0.30	0.88
lysosomal Pro-X carboxypeptidase isoform 1 preproprotein [Homo sapiens]	1.28	1.27	0.91	0.72
UV excision repair protein RAD23 homolog A isoform 1 [Homo sapiens]	0.64	0.18	0.14	0.80
RNA-binding protein 8A [Homo sapiens]	1.22	0.09	0.06	0.62
peptidoglycan recognition protein 1 precursor [Homo sapiens]	2.00	0.82	0.76	0.93
actin, alpha cardiac muscle 1 preproprotein [Homo sapiens]	0.88	0.12	0.12	1.00
carbonic anhydrase 3 [Homo sapiens]	1.47	0.68	0.88	1.30
chromatin assembly factor 1 subunit B [Homo sapiens]	1.69	3.15	3.75	1.19
calmodulin-like protein 3 [Homo sapiens]	0.78	0.73	0.50	0.74
neutrophil defensin 3 preproprotein [Homo sapiens]	1.41	0.11	0.10	0.92
glutamate dehydrogenase 1, mitochondrial precursor [Homo sapiens]	1.38	18.39	17.07	0.93
alanine aminotransferase 1 [Homo sapiens]	0.89	1.34	1.19	0.89
histone H1.3 [Homo sapiens]	2.68	0.06	0.75	12.67
histone H1.4 [Homo sapiens]	3.20	0.14	0.08	0.59
histone H1.5 [Homo sapiens]	2.19	0.04	0.65	15.41
histone H3.3 [Homo sapiens]	4.78	0.07	0.04	0.57
hemoglobin subunit zeta [Homo sapiens]	0.60	0.50	0.29	0.65
myoglobin [Homo sapiens]	1.74	3.05	3.26	1.07
tumor protein p73 isoform a [Homo sapiens]	0.56	0.30	0.11	0.50
alpha-centractin [Homo sapiens]	0.76	0.05	0.65	5.25
actin-related protein 2 isoform b [Homo sapiens]	0.78	0.06	0.07	1.18
actin-related protein 3 isoform 1 [Homo sapiens]	0.83	0.26	0.27	1.02
actin-related protein 2/3 complex subunit 5 isoform 1 [Homo sapiens]	0.84	0.26	0.23	0.88
actin-related protein 2/3 complex	0.88	0.13	0.11	0.85

subunit 4 isoform a [Homo sapiens]				
actin-related protein 2/3 complex				
subunit 2 [Homo sapiens]	0.89	0.25	0.24	0.94
cofilin-1 [Homo sapiens]	1.27	0.10	0.12	1.24
complement factor H-related protein				
2 precursor [Homo sapiens]	1.21	4.33	8.37	1.93
non-histone chromosomal protein				
HMG-17 [Homo sapiens]	1.63	0.35	0.11	0.33
inhibin beta C chain preproprotein				
[Homo sapiens]	0.88	3.54	2.50	0.71
L-lactate dehydrogenase A chain				
isoform 1 [Homo sapiens]	1.28	0.22	0.12	0.54
galectin-3-binding protein precursor				
[Homo sapiens]	1.74	5.58	4.65	0.83
lamin-B1 isoform 1 [Homo sapiens]	0.95	0.14	0.07	0.48
nicotinamide				
phosphoribosyltransferase precursor				
[Homo sapiens]	1.74	0.26	0.27	1.03
glycogen phosphorylase, muscle				
form isoform 1 [Homo sapiens]	1.24	0.52	0.51	0.97
protein S100-A11 [Homo sapiens]	1.87	0.15	0.20	1.34
protein S100-A12 [Homo sapiens]	2.40	0.11	0.08	0.73
CD5 antigen-like precursor [Homo				
sapiens]	1.52	1.19	1.79	1.50
malate dehydrogenase, cytoplasmic				
isoform 2 [Homo sapiens]	0.88	0.68	0.46	0.68
protein S100-A2 [Homo sapiens]	0.65	0.13	0.10	0.78
protein S100-P [Homo sapiens]	2.00	0.08	0.05	0.68
tubulin beta-4B chain [Homo				
sapiens]	0.96	0.26	0.28	1.10
noelin isoform 2 precursor [Homo				
sapiens]	1.31	2.18	1.79	0.82
peroxiredoxin-4 precursor [Homo				
sapiens]	0.89	0.35	0.35	1.01
GTP-binding nuclear protein Ran				
isoform 1 [Homo sapiens]	0.82	0.13	0.08	0.62
adenylyl cyclase-associated protein 2				
[Homo sapiens]	1.43	0.32	0.28	0.89
adenylyl cyclase-associated protein 1				
[Homo sapiens]	2.60	0.17	0.19	1.14
T-complex protein 1 subunit beta				
isoform 1 [Homo sapiens]	2.24	1.97	0.66	0.34
myosin regulatory light chain 12A				
[Homo sapiens]	0.82	0.15	0.19	1.29
acidic leucine-rich nuclear				
phosphoprotein 32 family member A				
[Homo sapiens]	0.88	0.23	0.23	1.03

serpin I2 isoform 2 precursor [Homo sapiens]	2.66	0.37	0.35	0.95
phospholipid transfer protein isoform a precursor [Homo sapiens]	1.27	1.68	1.43	0.85
14-3-3 protein sigma [Homo sapiens]	0.53	0.50	0.14	0.42
heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]	2.07	0.34	0.20	0.61
mannosyl-oligosaccharide 1,2-alpha-mannosidase IB [Homo sapiens]	1.58	14.72	13.92	0.95
nuclear migration protein nudC [Homo sapiens]	0.79	0.10	0.06	0.77
fibroblast growth factor precursor [Homo sapiens]	0.70	1.23	1.86	1.25
destrin isoform a [Homo sapiens]	1.90	0.11	0.07	0.68
N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase [Homo sapiens]	2.60	3.76	3.24	0.86
glutathione peroxidase 3 precursor [Homo sapiens]	2.79	5.89	7.37	1.25
cathepsin F precursor [Homo sapiens]	1.43	0.44	0.30	0.69
rab GDP dissociation inhibitor beta isoform 1 [Homo sapiens]	0.96	0.20	0.16	0.79
protocadherin-8 isoform 1 precursor [Homo sapiens]	1.35	8.14	5.20	0.64
hemoglobin subunit gamma-2 [Homo sapiens]	12.84	0.49	0.30	0.62
alpha-synuclein isoform NACP112 [Homo sapiens]	0.48	0.08	0.07	0.89
peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	0.92	0.44	0.32	0.71
granulocyte colony-stimulating factor [Homo sapiens]	0.91	0.07	0.05	0.73
histone H2A.V isoform 1 [Homo sapiens]	4.00	0.13	0.09	0.66
thyrotropin-releasing hormone-degrading ectoenzyme [Homo sapiens]	0.88	0.88	0.93	1.05
sex hormone-binding globulin isoform 1 precursor [Homo sapiens]	1.74	3.45	5.11	1.48
angiopoietin-related protein 3 preproprotein [Homo sapiens]	0.82	4.42	2.19	0.49
protein Z-dependent protease inhibitor precursor [Homo sapiens]	2.79	13.47	9.72	0.72
L-xylulose reductase isoform 1 [Homo sapiens]	0.73	1.43	1.54	0.99
alpha-hemoglobin-stabilizing protein [Homo sapiens]	0.81	1.12	0.96	0.85
protein CutA isoform 2 precursor [Homo sapiens]	0.70	0.13	0.18	1.16

carboxypeptidase Q preproprotein [Homo sapiens]	2.49	5.70	4.05	0.71
regulator of telomere elongation helicase 1 isoform 1 [Homo sapiens]	0.70	0.60	0.88	1.22
ficolin-1 precursor [Homo sapiens]	1.47	2.14	1.37	0.64
ficolin-2 isoform b precursor [Homo sapiens]	2.24	4.57	4.22	0.92
WD repeat-containing protein 1 isoform 1 [Homo sapiens]	2.60	0.38	0.32	0.84
tubulin alpha-8 chain isoform 1 [Homo sapiens]	0.77	0.14	0.15	0.96
UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 2 [Homo sapiens]	0.99	2.01	2.08	1.03
ras-related C3 botulinum toxin substrate 1 isoform Rac1b [Homo sapiens]	0.84	0.22	0.16	0.72
ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sapiens]	0.84	0.22	0.16	0.72
resistin precursor [Homo sapiens]	1.77	0.67	0.55	0.82
eukaryotic translation initiation factor 5A-2 [Homo sapiens]	0.99	0.26	0.23	0.88
endosialin precursor [Homo sapiens]	0.82	2.32	2.36	1.02
actin-related protein 3B isoform 1 [Homo sapiens]	0.82	0.22	0.19	0.86
alpha-amylase 2B precursor [Homo sapiens]	2.07	1.79	1.94	1.09
coagulation factor VII isoform b preproprotein [Homo sapiens]	0.88	4.76	4.39	0.92
calnexin precursor [Homo sapiens]	1.54	0.04	0.04	1.01
histone H2A type 1-D [Homo sapiens]	3.93	0.91	0.37	0.40
histone H2B type 1-B [Homo sapiens]	3.33	0.13	0.07	0.51
histone cluster 1, H2aj [Homo sapiens]	3.93	0.91	0.37	0.40
insulin-like growth factor-binding protein 5 precursor [Homo sapiens]	0.92	5.34	6.58	1.23
nucleophosmin isoform 1 [Homo sapiens]	1.58	0.42	0.32	0.76
pyruvate kinase PKLR isoform 1 [Homo sapiens]	1.28	0.21	0.19	0.90
plasminogen activator inhibitor 1 precursor [Homo sapiens]	1.22	2.48	2.33	0.94
apoptosis-associated speck-like protein containing a CARD isoform a [Homo sapiens]	1.19	0.25	0.20	0.82
thymosin beta-10 [Homo sapiens]	0.71	0.91	0.65	0.75

peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	1.58	0.28	0.21	0.75
lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	0.95	0.23	0.24	1.04
arginase-1 isoform 2 [Homo sapiens]	1.74	0.47	0.40	0.87
insulin-like growth factor I isoform 4 preproprotein [Homo sapiens]	1.28	7.34	8.34	1.14
thymosin beta-4 [Homo sapiens]	0.71	0.05	0.06	0.99
cytochrome c [Homo sapiens]	2.66	0.71	0.46	0.65
insulin-like growth factor-binding protein 6 precursor [Homo sapiens]	0.62	0.76	0.79	0.97
72 kDa type IV collagenase isoform a preproprotein [Homo sapiens]	0.50	1.49	1.30	0.86
azurocidin preproprotein [Homo sapiens]	2.46	0.31	0.27	0.85
prosaposin isoform a preproprotein [Homo sapiens]	1.77	0.29	0.35	1.22
nectin-3 isoform 1 precursor [Homo sapiens]	1.28	6.44	6.36	0.99
fibrinogen alpha chain isoform alpha preproprotein [Homo sapiens]	1.35	0.14	0.13	0.95
alpha-actinin-4 [Homo sapiens]	0.88	0.28	0.21	0.76
COP9 signalosome complex subunit 7b isoform b [Homo sapiens]	0.67	7.11	6.15	0.86
calpain-1 catalytic subunit [Homo sapiens]	0.97	0.52	0.53	1.03
myosin-9 [Homo sapiens]	2.79	0.07	0.05	0.72
myosin-11 isoform SM2A [Homo sapiens]	1.28	0.14	0.15	1.05
myosin-11 isoform SM1A [Homo sapiens]	1.28	0.14	0.15	1.05
sulfhydryl oxidase 1 isoform a precursor [Homo sapiens]	0.88	2.44	2.45	1.00
tubulin alpha chain-like 3 isoform 1 [Homo sapiens]	0.77	0.04	0.70	6.92
immunoglobulin lambda-like polypeptide 1 isoform a precursor [Homo sapiens]	2.49	0.30	2.16	7.19
desmocollin-1 isoform Dsc1a preproprotein [Homo sapiens]	2.49	4.21	3.19	0.76
desmocollin-2 isoform Dsc2a preproprotein [Homo sapiens]	1.00	1.71	1.83	1.07
desmocollin-2 isoform Dsc2b preproprotein [Homo sapiens]	1.00	1.71	1.83	1.07
complement factor H-related protein 5 precursor [Homo sapiens]	0.97	1.33	2.16	1.62
complement C1q tumor necrosis factor-related protein 3 isoform a	0.96	1.80	1.43	0.80

precursor [Homo sapiens]				
heat shock-related 70 kDa protein 2 [Homo sapiens]	2.24	0.34	0.19	0.55
SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]	0.73	0.17	0.15	0.85
beta-1,4-galactosyltransferase 1 [Homo sapiens]	0.88	4.33	4.15	0.96
heterogeneous nuclear ribonucleoprotein M isoform a [Homo sapiens]	0.92	0.85	0.46	0.54
exostosin-like 2 isoform 1 [Homo sapiens]	0.83	8.27	8.34	1.01
calpain small subunit 2 [Homo sapiens]	2.07	0.26	0.24	0.91
heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]	0.95	0.30	0.27	0.90
heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]	0.95	0.30	0.27	0.90
alpha-internexin [Homo sapiens]	1.00	0.35	0.44	1.26
transcription elongation factor A protein-like 3 [Homo sapiens]	1.50	0.85	0.04	0.04
N-acetylglucosamine-1-phosphotransferase subunit gamma precursor [Homo sapiens]	1.74	11.66	11.04	0.95
tubulin alpha-1C chain [Homo sapiens]	0.81	0.08	0.08	1.18
complement C2 isoform 1 preproprotein [Homo sapiens]	1.74	4.37	5.53	1.27
cadherin-2 preproprotein [Homo sapiens]	0.97	2.10	1.86	0.89
cadherin-3 preproprotein [Homo sapiens]	0.83	2.92	2.17	0.74
protocadherin-8 isoform 2 precursor [Homo sapiens]	1.35	8.14	5.20	0.64
kelch-like protein 1 isoform 1 [Homo sapiens]	0.32	0.26		
mimecan preproprotein [Homo sapiens]	0.79	0.78	2.39	1.99
granzyme H isoform 1 precursor [Homo sapiens]	0.82	1.24	1.34	1.08
histidine protein methyltransferase 1 homolog [Homo sapiens]	0.74	0.11	0.04	0.53
histone H2A type 3 [Homo sapiens]	3.93	0.91	0.37	0.40
inactive tyrosine-protein kinase 7 isoform a precursor [Homo sapiens]	0.88	1.42	1.41	0.99
selenium-binding protein 1 isoform 1	0.63	0.35	0.21	0.68

[Homo sapiens]				
histone H2B type 1-O [Homo sapiens]	3.33	0.13	0.07	0.51
leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	1.22	10.24	14.07	1.37
78 kDa glucose-regulated protein precursor [Homo sapiens]	1.26	2.45	1.98	0.81
protein Wnt-6 precursor [Homo sapiens]	3.40	14.41	4.53	0.31
dermcidin preproprotein [Homo sapiens]	0.88	0.18	0.23	1.27
seprase isoform 1 [Homo sapiens]	1.40	15.36	15.15	0.99
fibronectin isoform 3 preproprotein [Homo sapiens]	2.60	5.92	2.31	0.39
argininosuccinate synthase [Homo sapiens]	0.79	1.26	0.77	0.68
noelin isoform 1 precursor [Homo sapiens]	1.27	2.18	2.46	1.13
peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapiens]	0.77	0.17	0.16	0.92
roundabout homolog 4 precursor [Homo sapiens]	0.73	0.46	0.41	0.87
tubulin alpha-4A chain isoform 1 [Homo sapiens]	0.77	0.14	0.15	0.96
tubulin alpha-3C/D chain [Homo sapiens]	0.77	0.14	0.15	0.96
major histocompatibility complex, class I, B precursor [Homo sapiens]	0.81	1.42	1.65	1.43
myosin light polypeptide 6 isoform 1 [Homo sapiens]	0.78	0.12	0.12	0.94
tyrosine-protein phosphatase non-receptor type 6 isoform 1 [Homo sapiens]	0.64	0.18	0.15	0.82
tyrosine-protein phosphatase non-receptor type 6 isoform 2 [Homo sapiens]	0.64	0.18	0.15	0.82
tyrosine-protein phosphatase non-receptor type 6 isoform 3 [Homo sapiens]	0.64	0.18	0.15	0.82
histone H2A type 1-H [Homo sapiens]	3.93	0.91	0.37	0.40
histone H2B type 1-K [Homo sapiens]	3.33	0.13	0.07	0.51
vascular cell adhesion protein 1 isoform b precursor [Homo sapiens]	1.43	4.59	5.51	1.20
asialoglycoprotein receptor 2 isoform b [Homo sapiens]	0.83	4.65	4.50	0.97
asialoglycoprotein receptor 2 isoform c [Homo sapiens]	0.83	4.65	4.50	0.97

dipeptidyl peptidase 4 [Homo sapiens]	1.58	3.47	3.47	1.00
dynein heavy chain 5, axonemal [Homo sapiens]	0.76	0.28	0.28	0.94
histone H2A type 1-B/E [Homo sapiens]	3.93	0.91	0.37	0.40
V-type proton ATPase subunit B, kidney isoform [Homo sapiens]	0.60	0.26	0.29	1.58
V-type proton ATPase subunit B, brain isoform [Homo sapiens]	0.60	0.26	0.29	1.58
serum paraoxonase/arylesterase 1 precursor [Homo sapiens]	0.57	0.52	0.56	1.00
hsc70-interacting protein isoform 1 [Homo sapiens]	0.84	0.47	0.37	0.79
nuclear autoantigen Sp-100 isoform 2 [Homo sapiens]	1.19	0.06	0.06	0.94
multiple inositol polyphosphate phosphatase 1 isoform 1 precursor [Homo sapiens]	1.31	14.72	11.81	0.80
protein disulfide-isomerase precursor [Homo sapiens]	0.84	0.63	0.56	0.89
nucleobindin-1 precursor [Homo sapiens]	0.64	0.22	0.12	0.64
endomucin isoform 1 precursor [Homo sapiens]	1.31	10.71	15.71	1.47
bifunctional purine biosynthesis protein PURH [Homo sapiens]	1.26	0.27	0.22	0.79
glycogenin-1 isoform 1 [Homo sapiens]	1.26	0.17	0.37	2.18
ferritin light chain [Homo sapiens]	1.52	0.46	0.44	0.96
proline-serine-threonine phosphatase-interacting protein 1 [Homo sapiens]	0.88	0.04	0.93	24.95
NSFL1 cofactor p47 isoform a [Homo sapiens]	0.78	0.44	0.34	0.80
EF-hand domain-containing protein D2 [Homo sapiens]	0.97	0.11	0.10	0.90
histone H2B type 1-D [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2B type 1-J [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2A.V isoform 2 [Homo sapiens]	4.00	0.13	0.09	0.66
tenascin-X isoform 2 [Homo sapiens]	0.95	2.91	5.08	1.75
alpha-1B-glycoprotein precursor [Homo sapiens]	1.28	6.70	7.10	1.06
beta-Ala-His dipeptidase precursor [Homo sapiens]	1.58	5.66	7.87	1.39
histone H2B type 1-C/E/F/G/I [Homo sapiens]	3.33	0.13	0.07	0.51

sapiens]				
scaffold attachment factor B1				
isoform 3 [Homo sapiens]	1.41	0.78	0.49	0.63
peripherin [Homo sapiens]	0.62	0.09	0.08	0.85
mannan-binding lectin serine				
protease 1 isoform 1 precursor				
[Homo sapiens]	0.92	1.55	1.56	1.00
mannan-binding lectin serine				
protease 1 isoform 2 precursor				
[Homo sapiens]	0.97	3.89	3.87	1.00
mannan-binding lectin serine				
protease 2 isoform 2 precursor				
[Homo sapiens]	1.28	6.99	5.11	0.73
mannan-binding lectin serine				
protease 2 isoform 1 preproprotein				
[Homo sapiens]	2.60	5.23	3.82	0.73
A disintegrin and metalloproteinase				
with thrombospondin motifs 13				
isoform 1 preproprotein [Homo				
sapiens]	2.07	3.41	3.63	1.07
A disintegrin and metalloproteinase				
with thrombospondin motifs 13				
isoform 3 preproprotein [Homo				
sapiens]	2.07	3.41	3.63	1.07
kallikrein-7 isoform 1 preproprotein				
[Homo sapiens]	1.58	0.41	0.99	2.40
retinal dehydrogenase 1 [Homo				
sapiens]	0.74	0.37	0.21	0.65
serine/arginine-rich splicing factor 4				
[Homo sapiens]	0.82	0.39		
tubulin beta-4A chain isoform 3				
[Homo sapiens]	0.77	0.18	0.14	0.78
glycogen phosphorylase, brain form				
[Homo sapiens]	1.29	0.39	0.41	1.05
phosphoglucomutase-1 isoform 1				
[Homo sapiens]	1.90	0.65	0.38	0.59
protein disulfide-isomerase A3				
precursor [Homo sapiens]	0.93	0.60	0.56	0.94
drebrin-like protein isoform a [Homo				
sapiens]	0.88	0.50	0.51	1.02
ELL-associated factor 2 [Homo				
sapiens]	2.44	0.18	0.13	0.71
PITH domain-containing protein 1				
[Homo sapiens]	0.79	0.04	0.65	6.58
stathmin-4 isoform 1 [Homo sapiens]	0.84	0.15	0.09	0.60
junctional sarcoplasmic reticulum				
protein 1 [Homo sapiens]	3.44	10.70	14.17	1.32
atractin isoform 1 preproprotein	0.84	2.47	5.16	2.09

[Homo sapiens]				
attractin isoform 2 preproprotein				
[Homo sapiens]	0.84	2.47	5.16	2.09
14-3-3 protein gamma [Homo sapiens]	0.67	0.22	0.21	0.92
creatine kinase B-type [Homo sapiens]	0.57	0.53	0.74	1.18
creatine kinase M-type [Homo sapiens]	0.68	0.69	0.90	1.13
trypsin-3 isoform 2 preproprotein [Homo sapiens]	0.76	0.63	0.62	0.93
protein S100-A8 [Homo sapiens]	3.33	0.13	0.15	1.16
coactosin-like protein [Homo sapiens]	0.88	0.17	0.18	1.03
zinc transporter 6 isoform 2 [Homo sapiens]	0.71	1.93	1.82	0.98
apolipoprotein L1 isoform a precursor [Homo sapiens]	0.62	0.68	0.56	0.84
apolipoprotein L1 isoform b precursor [Homo sapiens]	0.62	0.68	0.56	0.84
myotrophin [Homo sapiens]	0.96	0.19	0.21	1.08
amyloid beta A4 precursor protein-binding family B member 1 isoform b [Homo sapiens]	2.49	43.95	58.97	1.34
apoptosis-associated speck-like protein containing a CARD isoform b [Homo sapiens]	1.19	0.25	0.20	0.82
apolipoprotein M isoform 1 [Homo sapiens]	0.70	2.49	1.23	0.59
annexin A11 isoform 1 [Homo sapiens]	1.54	0.36	0.39	1.08
cathepsin Z preproprotein [Homo sapiens]	1.22	1.49	1.19	0.80
proteasome subunit beta type-4 [Homo sapiens]	0.65	0.51	0.54	0.98
oncoprotein-induced transcript 3 protein precursor [Homo sapiens]	0.95	1.67	1.79	1.07
inactive tyrosine-protein kinase 7 isoform b precursor [Homo sapiens]	0.88	1.42	1.41	0.99
inactive tyrosine-protein kinase 7 isoform c precursor [Homo sapiens]	0.88	1.42	1.41	0.99
inactive tyrosine-protein kinase 7 isoform d precursor [Homo sapiens]	0.88	1.42	1.41	0.99
proteasome subunit beta type-6 isoform 1 proprotein [Homo sapiens]	0.97	0.53	0.48	0.91
proteasome subunit alpha type-1 isoform 1 [Homo sapiens]	0.68	0.83	0.75	0.88
proteasome subunit alpha type-3	0.89	0.73	0.67	0.92

isoform 2 [Homo sapiens]				
proteasome subunit alpha type-5				
isoform 1 [Homo sapiens]	0.88	2.07	1.19	0.58
proteasome subunit alpha type-6				
isoform a [Homo sapiens]	0.88	0.16	0.20	1.22
cathepsin S isoform 1 preproprotein				
[Homo sapiens]	1.55	0.59	0.61	1.02
angiotensin-converting enzyme				
isoform 2 precursor [Homo sapiens]	1.28	5.38	4.78	0.89
acylamino-acid-releasing enzyme				
[Homo sapiens]	0.74	0.26	0.20	0.81
tropomyosin alpha-3 chain isoform 2				
[Homo sapiens]	1.35	0.21	0.20	0.97
heat shock cognate 71 kDa protein				
isoform 2 [Homo sapiens]	2.07	0.36	0.25	0.70
adipocyte plasma membrane-				
associated protein [Homo sapiens]	0.76	0.34	0.40	1.54
keratin, type I cytoskeletal 16 [Homo				
sapiens]	0.45	0.11	0.07	0.74
mannosyl-oligosaccharide 1,2-alpha-				
mannosidase IA [Homo sapiens]	0.96	4.04	4.06	1.00
histone H2B type 1-A [Homo sapiens]	3.48	0.11	0.06	0.50
histone H2A type 2-C [Homo sapiens]	3.93	0.91	0.37	0.40
HLA class I histocompatibility				
antigen, A-1 alpha chain precursor				
[Homo sapiens]	0.81	2.02	2.41	1.63
histone H2A type 1-A [Homo				
sapiens]	3.93	0.91	0.37	0.40
26S proteasome non-ATPase				
regulatory subunit 3 [Homo sapiens]	2.49	0.26	0.16	0.63
S-phase kinase-associated protein 1				
isoform b [Homo sapiens]	0.52	0.14	0.11	0.84
lamin isoform A [Homo sapiens]	0.76	0.30	0.20	0.71
lamin isoform A-delta10 [Homo				
sapiens]	0.76	0.30	0.20	0.71
ficolin-3 isoform 1 precursor [Homo				
sapiens]	2.79	5.66	7.03	1.24
ficolin-3 isoform 2 precursor [Homo				
sapiens]	2.79	5.31	5.12	0.97
calpastatin isoform b [Homo sapiens]	0.58	0.26	0.24	0.88
serpin B4 [Homo sapiens]	0.74	0.17	0.17	0.95
histone H2B type 3-B [Homo sapiens]	3.33	0.13	0.07	0.51
histone H2A type 2-B [Homo sapiens]	3.93	0.91	0.37	0.40
hemoglobin subunit gamma-1				
[Homo sapiens]	15.79	0.46	0.39	0.85
contactin-1 isoform 1 precursor				
[Homo sapiens]	1.58	3.13	3.22	1.03

contactin-1 isoform 2 precursor [Homo sapiens]	1.58	3.13	3.22	1.03
unconventional myosin-XVIIIa isoform a [Homo sapiens]	1.63	0.91	0.41	0.45
laminin subunit alpha-2 isoform a precursor [Homo sapiens]	0.70	4.20	3.24	0.79
interleukin-6 receptor subunit beta isoform 1 precursor [Homo sapiens]	0.68	0.74	0.63	0.84
interleukin-6 receptor subunit beta isoform 2 precursor [Homo sapiens]	0.68	0.74	0.63	0.84
dual oxidase 1 precursor [Homo sapiens]	0.81	0.30	0.24	0.82
phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapiens]	0.70	1.54	1.45	0.95
Golgi membrane protein 1 [Homo sapiens]	0.91	3.13	2.29	0.73
histone H2A.J [Homo sapiens]	3.93	0.91	0.37	0.40
NSFL1 cofactor p47 isoform b [Homo sapiens]	0.78	0.44	0.34	0.80
myosin regulatory light polypeptide 9 isoform a [Homo sapiens]	0.88	0.25	0.39	1.58
epidermal growth factor receptor isoform a precursor [Homo sapiens]	0.92	3.80	3.69	0.97
serine/threonine-protein phosphatase 2A activator isoform b [Homo sapiens]	0.89	0.26	0.16	0.64
tubulin beta-2B chain [Homo sapiens]	1.27	0.26	0.28	1.10
tubulin beta chain isoform b [Homo sapiens]	0.83	0.12	0.11	0.92
eukaryotic translation initiation factor 2 subunit 2 [Homo sapiens]	1.54	0.56	0.21	0.38
proteasome activator complex subunit 2 [Homo sapiens]	1.40	0.44	0.33	0.74
out at first protein homolog precursor [Homo sapiens]	2.60	6.47	5.95	0.92
trem-like transcript 1 protein isoform a precursor [Homo sapiens]	0.92	4.26	5.57	1.31
proprotein convertase subtilisin/kexin type 9 preproprotein [Homo sapiens]	0.97	6.68	6.67	1.00
glutamate dehydrogenase 2, mitochondrial precursor [Homo sapiens]	1.38	18.39	17.07	0.93
polymeric immunoglobulin receptor precursor [Homo sapiens]	0.91	2.52	2.28	0.90
argininosuccinate lyase isoform 1	1.54	1.41	2.71	1.92

[Homo sapiens]				
glycogen [starch] synthase, muscle isoform 1 [Homo sapiens]	1.31	0.04	0.65	16.31
inter-alpha-trypsin inhibitor heavy chain H4 isoform 1 precursor [Homo sapiens]	1.74	6.35	5.98	0.94
phosphoglycerate kinase 2 [Homo sapiens]	0.97	0.10	0.08	0.83
thrombospondin-4 precursor [Homo sapiens]	1.37	1.71	1.77	1.04
tumor protein 63 isoform 1 [Homo sapiens]	0.56	0.30	0.11	0.50
myosin regulatory light polypeptide 9 isoform b [Homo sapiens]	0.88	0.25	0.39	1.58
lipopolysaccharide-binding protein precursor [Homo sapiens]	1.40	6.35	11.00	1.73
apolipoprotein C-II precursor [Homo sapiens]	0.95	7.76	5.94	0.77
prostaglandin-H2 D-isomerase precursor [Homo sapiens]	0.91	3.53	3.18	0.90
peroxiredoxin-2 [Homo sapiens]	0.66	0.13	0.07	0.63
olfactomedin-4 precursor [Homo sapiens]	8.68	0.68	0.69	1.01
peroxiredoxin-5, mitochondrial isoform b precursor [Homo sapiens]	0.76	0.23	0.18	0.79
peroxiredoxin-5, mitochondrial isoform c precursor [Homo sapiens]	0.88	0.37	0.32	0.86
peroxiredoxin-1 [Homo sapiens]	0.88	0.30	0.24	0.79
neurofilament heavy polypeptide [Homo sapiens]	1.00	0.35	0.44	1.26
keratin, type II cytoskeletal 79 [Homo sapiens]	0.73	0.35	0.69	1.49
pyruvate kinase PKLR isoform 2 [Homo sapiens]	1.28	0.21	0.19	0.90
glutathione peroxidase 6 precursor [Homo sapiens]	1.76	18.04	23.27	1.29
pyruvate kinase PKM isoform b [Homo sapiens]	1.00	0.19	0.18	0.94
opioid growth factor receptor [Homo sapiens]	1.69	0.21	0.11	0.50
phospholipid transfer protein isoform b precursor [Homo sapiens]	1.27	1.68	1.43	0.85
podocalyxin isoform 2 precursor [Homo sapiens]	2.49	1.19	0.98	0.82
target of Nesh-SH3 precursor [Homo sapiens]	0.82	2.55	1.58	0.62
cofilin-2 isoform 1 [Homo sapiens]	1.19	0.08	0.07	0.91
nuclease-sensitive element-binding	2.24	0.05	0.98	19.85

protein 1 [Homo sapiens]				
ras-related protein Rab-7a [Homo sapiens]	1.74	0.40	0.41	1.04
endothelial protein C receptor precursor [Homo sapiens]	0.99	9.42	6.92	0.73
heat shock 70 kDa protein 6 [Homo sapiens]	2.24	0.10	0.12	1.24
alcohol dehydrogenase 1B isoform 1 [Homo sapiens]	0.92	1.79	0.65	0.36
fibulin-1 isoform C precursor [Homo sapiens]	0.95	1.13	1.31	1.15
fibulin-1 isoform D precursor [Homo sapiens]	0.95	2.48	1.96	0.79
stathmin-2 isoform 2 [Homo sapiens]	0.83	0.18	0.13	0.74
synaptonemal complex protein 1 isoform 1 [Homo sapiens]	1.28	3.61	3.63	1.01
ADP-sugar pyrophosphatase [Homo sapiens]	0.97	2.20	1.89	0.86
ADAMTS-like protein 4 isoform 1 precursor [Homo sapiens]	1.58	8.41	6.97	0.83
erythrocyte band 7 integral membrane protein isoform a [Homo sapiens]	1.29	0.10	0.08	0.83
complement C5 preproprotein [Homo sapiens]	1.74	5.60	6.53	1.17
nucleoside diphosphate kinase A isoform a [Homo sapiens]	0.95	0.18	0.13	0.74
ribonuclease pancreatic precursor [Homo sapiens]	0.96	1.48	1.60	1.08
neutral alpha-glucosidase AB isoform 2 precursor [Homo sapiens]	2.49	0.73	0.51	0.71
heat shock 70 kDa protein 4 [Homo sapiens]	0.97	0.06	0.04	0.76
suprabasin isoform 2 precursor [Homo sapiens]	0.48	0.90	0.77	0.85
neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	2.24	0.30	0.22	0.74
serpin B8 isoform a [Homo sapiens]	2.66	0.37	0.35	0.95
ATP-citrate synthase isoform 2 [Homo sapiens]	0.99	0.78	0.63	0.81
pigment epithelium-derived factor precursor [Homo sapiens]	2.49	11.87	12.51	1.05
semaphorin-4B precursor [Homo sapiens]	2.60	2.53	2.33	0.92
plasma alpha-L-fucosidase precursor [Homo sapiens]	0.82	5.25	2.24	0.43
6-phosphogluconate dehydrogenase, decarboxylating [Homo sapiens]	0.99	0.18	0.13	0.72

cartilage oligomeric matrix protein precursor [Homo sapiens]	2.49	4.59	3.71	0.81
pre-mRNA 3'-end-processing factor FIP1 isoform 1 [Homo sapiens]	3.12	0.26	0.22	0.86
plexin domain-containing protein 2 isoform 1 precursor [Homo sapiens]	0.88	2.19	2.08	0.95
coiled-coil domain-containing protein 126 precursor [Homo sapiens]	0.97	16.78	15.96	0.95
thrombospondin-1 precursor [Homo sapiens]	1.28	5.16	4.89	0.95
thrombospondin-2 precursor [Homo sapiens]	1.00	0.80	0.82	1.03
nucleophosmin isoform 2 [Homo sapiens]	1.58	0.42	0.32	0.76
bisphosphoglycerate mutase [Homo sapiens]	0.70	0.42	0.31	0.78
fructose-bisphosphate aldolase B [Homo sapiens]	1.28	4.03	3.23	0.80
lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [Homo sapiens]	1.00	10.26	6.21	0.61
ubiquitin-conjugating enzyme E2 variant 1 isoform a [Homo sapiens]	0.84	0.10	0.13	1.33
TMEM189-UBE2V1 fusion protein [Homo sapiens]	0.84	0.10	0.13	1.33
cytochrome b5 isoform 1 [Homo sapiens]	0.79	0.45	0.34	0.79
plectin isoform 1e [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1d [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1f [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1g [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1 [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1b [Homo sapiens]	1.37	0.35	0.27	0.76
plectin isoform 1a [Homo sapiens]	1.37	0.35	0.27	0.76
calponin-2 isoform b [Homo sapiens]	0.71	0.17	0.15	0.87
epidermal growth factor receptor isoform b precursor [Homo sapiens]	0.92	3.80	3.69	0.97
epidermal growth factor receptor isoform c precursor [Homo sapiens]	0.92	3.80	3.69	0.97
epidermal growth factor receptor isoform d precursor [Homo sapiens]	0.92	3.80	3.69	0.97
amyloid beta A4 protein isoform b precursor [Homo sapiens]	0.99	6.19	3.99	0.65
amyloid beta A4 protein isoform c precursor [Homo sapiens]	0.99	3.59	3.36	0.94
histone H2A.V isoform 3 [Homo sapiens]	4.00	0.13	0.09	0.66

sapiens]				
histone H2A.V isoform 5 [Homo sapiens]	4.00	0.13	0.09	0.66
immunoglobulin superfamily containing leucine-rich repeat protein precursor [Homo sapiens]	0.91	2.44	2.41	0.99
tropomyosin beta chain isoform 1 [Homo sapiens]	2.79	0.77	0.63	0.82
trans-Golgi network integral membrane protein 2 isoform 1 precursor [Homo sapiens]	1.43	11.66	11.58	0.99
vacuolar protein sorting-associated protein 13C isoform 1A [Homo sapiens]	0.88	1.56	0.32	0.21
complement factor D preproprotein [Homo sapiens]	0.88	3.67	3.30	0.90
tubulin beta-8 chain [Homo sapiens]	0.96	0.62	0.49	0.78
protein FAM49B [Homo sapiens]	0.89	0.46	0.50	1.10
hepatocyte growth factor receptor isoform b precursor [Homo sapiens]	1.28	1.17	2.08	1.78
unconventional myosin-XVIIIa isoform b [Homo sapiens]	1.63	0.91	0.41	0.45
stathmin isoform a [Homo sapiens]	0.89	0.18	0.12	0.69
eosinophil cationic protein precursor [Homo sapiens]	3.10	0.30	0.35	1.15
multimerin-1 precursor [Homo sapiens]	0.99	3.82	3.57	0.94
growth factor receptor-bound protein 2 isoform 2 [Homo sapiens]	0.96	0.48	0.49	1.01
complement component C7 precursor [Homo sapiens]	0.93	5.45	5.18	0.95
haptoglobin-related protein precursor [Homo sapiens]	0.73	0.41	0.49	1.59
limbic system-associated membrane protein preproprotein [Homo sapiens]	2.07	3.04	2.37	0.78
serglycin precursor [Homo sapiens]	1.27	5.98	6.31	1.06
parathymosin [Homo sapiens]	0.74	0.41	0.15	0.49
alpha-endosulfine isoform 1 [Homo sapiens]	1.19	0.07	0.09	1.20
alpha-endosulfine isoform 2 [Homo sapiens]	1.19	0.07	0.09	1.20
alpha-endosulfine isoform 4 [Homo sapiens]	1.19	0.07	0.09	1.20
alpha-endosulfine isoform 8 [Homo sapiens]	1.19	0.07	0.09	1.20
tubulin alpha-3E chain [Homo sapiens]	0.71	0.28	0.25	0.88

attractin-like protein 1 isoform 1 precursor [Homo sapiens]	0.68	1.77	2.36	1.14
fibronectin isoform 7 preproprotein [Homo sapiens]	0.99	5.11	1.92	0.38
fibronectin isoform 6 preproprotein [Homo sapiens]	2.60	5.94	2.30	0.39
fibronectin isoform 5 preproprotein [Homo sapiens]	2.60	5.94	2.31	0.39
fibronectin isoform 4 preproprotein [Homo sapiens]	2.60	5.94	2.30	0.39
fibronectin isoform 1 preproprotein [Homo sapiens]	2.60	5.94	2.31	0.39
keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	0.34	0.21	0.30	1.18
tropomyosin beta chain isoform 2 [Homo sapiens]	2.79	0.77	0.63	0.82
plectin isoform 1c [Homo sapiens]	1.37	0.35	0.27	0.76
cartilage acidic protein 1 isoform A precursor [Homo sapiens]	0.88	2.32	2.65	1.14
alpha-soluble NSF attachment protein [Homo sapiens]	0.64	0.32	0.30	0.92
glucosidase 2 subunit beta isoform 1 precursor [Homo sapiens]	1.52	0.80	0.76	0.95
non-histone chromosomal protein HMG-14 [Homo sapiens]	1.26	0.39	0.18	0.45
CD44 antigen isoform 1 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 2 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 3 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 4 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 5 precursor [Homo sapiens]	2.60	3.80	3.20	0.84
UTP--glucose-1-phosphate uridylyltransferase isoform a [Homo sapiens]	0.99	0.78	0.52	0.67
collagen alpha-2(I) chain precursor [Homo sapiens]	0.50	0.40	0.30	0.79
eukaryotic translation initiation factor 3 subunit G [Homo sapiens]	0.81	3.89	2.36	0.68
protein YIPF3 [Homo sapiens]	0.93	2.39	2.44	1.02
matrix Gla protein isoform 2 precursor [Homo sapiens]	1.74	3.38	4.84	1.43
glutathione reductase, mitochondrial isoform 1 precursor [Homo sapiens]	2.60	1.11	1.00	0.90
alpha-1-antitrypsin precursor [Homo sapiens]	1.43	14.24	10.12	0.71

sapiens]				
low affinity immunoglobulin gamma Fc region receptor II-a isoform 2 precursor [Homo sapiens]	0.81	1.41	1.51	0.99
thioredoxin isoform 1 [Homo sapiens]	1.43	0.25	0.18	0.74
tubulin beta-3 chain isoform 1 [Homo sapiens]	1.27	0.26	0.28	1.10
phosphoglycerate mutase 2 [Homo sapiens]	0.97	0.52	0.41	0.80
alpha-1-antichymotrypsin precursor [Homo sapiens]	2.49	10.14	12.14	1.20
low affinity immunoglobulin gamma Fc region receptor III-A isoform a precursor [Homo sapiens]	2.19	3.58	5.49	1.53
annexin A2 isoform 1 [Homo sapiens]	1.74	0.19	0.20	1.03
probable peptidyl-tRNA hydrolase [Homo sapiens]	0.88	2.30	1.76	0.76
alpha-mannosidase 2 [Homo sapiens]	1.40	5.35	4.37	0.82
sulfhydryl oxidase 1 isoform b precursor [Homo sapiens]	0.88	2.50	2.49	1.00
endoplasmic reticulum resident protein 44 precursor [Homo sapiens]	1.43	2.39	2.71	1.13
HLA class I histocompatibility antigen, Cw-1 alpha chain precursor [Homo sapiens]	0.99	0.65	1.18	1.83
WD repeat-containing protein 1 isoform 2 [Homo sapiens]	2.60	0.39	0.37	0.95
histone H3.2 [Homo sapiens]	3.42	0.08	0.05	0.62
voltage-dependent calcium channel subunit alpha-2/delta-1 precursor [Homo sapiens]	1.28	3.53	3.91	1.11
voltage-dependent calcium channel subunit alpha-2/delta-2 isoform a precursor [Homo sapiens]	2.49	11.30	11.75	1.04
voltage-dependent calcium channel subunit alpha-2/delta-2 isoform b precursor [Homo sapiens]	2.49	11.30	11.75	1.04
lactotransferrin isoform 1 precursor [Homo sapiens]	1.57	0.10	0.08	0.83
Golgi apparatus protein 1 isoform 1 precursor [Homo sapiens]	1.35	13.31	9.67	0.73
complement factor H-related protein 3 isoform 1 precursor [Homo sapiens]	0.88	3.51	2.67	0.76
kinase D-interacting substrate of 220	0.67	0.05	0.06	1.38

kDa [Homo sapiens]				
RNA-binding protein 25 [Homo sapiens]	0.57	0.22	0.14	0.69
collagen alpha-3(VI) chain isoform 1 precursor [Homo sapiens]	0.79	2.59	1.51	0.66
collagen alpha-3(VI) chain isoform 5 precursor [Homo sapiens]	0.79	2.59	1.51	0.66
retinol-binding protein 4 precursor [Homo sapiens]	1.18	9.18	10.84	1.18
desmin [Homo sapiens]	0.82	0.22	0.19	0.86
C-reactive protein precursor [Homo sapiens]	2.60	3.38	6.95	2.06
insulin-like growth factor-binding protein 2 precursor [Homo sapiens]	0.79	3.97	3.52	0.87
RWD domain-containing protein 1 isoform a [Homo sapiens]	1.58	0.04	0.93	22.23
RWD domain-containing protein 1 isoform b [Homo sapiens]	1.58	0.04	0.93	22.23
keratin, type I cytoskeletal 9 [Homo sapiens]	0.55	1.09	0.70	0.71
nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 [Homo sapiens]	6.20	0.31	0.16	0.52
transgelin-3 [Homo sapiens]	0.83	0.40	0.20	0.51
putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform 2 [Homo sapiens]	0.96	0.31	0.32	1.04
rho GDP-dissociation inhibitor 2 [Homo sapiens]	0.88	0.12	0.11	0.92
ferritin heavy chain [Homo sapiens]	0.99	0.57	0.52	0.92
complement C1q subcomponent subunit C precursor [Homo sapiens]	0.99	5.67	5.89	1.04
cyclic AMP-dependent transcription factor ATF-6 alpha [Homo sapiens]	1.43	4.67	3.87	0.83
ADAMTS-like protein 4 isoform 2 precursor [Homo sapiens]	1.58	8.41	6.97	0.83
tubulin alpha-1B chain [Homo sapiens]	0.81	0.08	0.08	1.18
von Willebrand factor A domain-containing protein 8 isoform a precursor [Homo sapiens]	1.79	26.69	17.45	0.65
von Willebrand factor A domain-containing protein 8 isoform b precursor [Homo sapiens]	1.79	26.69	17.45	0.65
calmodulin [Homo sapiens]	1.52	0.08	0.05	0.68
serrate RNA effector molecule homolog isoform a [Homo sapiens]	1.74	2.91	2.80	0.96
fetuin-B precursor [Homo sapiens]	0.96	5.10	3.83	0.75

destrin isoform b [Homo sapiens]	1.90	0.11	0.07	0.68
heterogeneous nuclear ribonucleoprotein A1-like 2 [Homo sapiens]	0.73	0.07	0.04	0.75
serpin I2 isoform 1 precursor [Homo sapiens]	2.66	0.37	0.35	0.95
retina-specific copper amine oxidase isoform a precursor [Homo sapiens]	1.27	3.60	3.89	1.08
retina-specific copper amine oxidase isoform b precursor [Homo sapiens]	1.27	3.60	3.89	1.08
putative ubiquitin-conjugating enzyme E2 N-like [Homo sapiens]	0.88	0.85	0.32	0.38
ficolin-2 isoform a precursor [Homo sapiens]	2.07	4.59	4.58	1.00
4F2 cell-surface antigen heavy chain isoform b [Homo sapiens]	0.82	1.55	1.34	0.87
4F2 cell-surface antigen heavy chain isoform e [Homo sapiens]	0.82	1.55	1.34	0.87
4F2 cell-surface antigen heavy chain isoform f [Homo sapiens]	0.82	1.55	1.34	0.87
drebrin-like protein isoform b [Homo sapiens]	0.88	0.50	0.51	1.02
protein CutA isoform 1 [Homo sapiens]	0.70	0.13	0.18	1.16
insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]	0.96	4.63	4.99	1.08
insulin-like growth factor-binding protein 3 isoform a precursor [Homo sapiens]	0.96	4.63	4.99	1.08
insulin-like growth factor-binding protein 4 precursor [Homo sapiens]	0.83	1.71	1.56	0.91
complement C1q tumor necrosis factor-related protein 3 isoform b precursor [Homo sapiens]	0.96	1.80	1.43	0.80
complement factor H isoform a precursor [Homo sapiens]	0.99	5.66	6.21	1.10
complement factor H isoform b precursor [Homo sapiens]	0.63	0.37	0.40	1.37
C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	1.43	8.81	9.18	1.04
HLA class I histocompatibility antigen, alpha chain E precursor [Homo sapiens]	0.81	2.02	2.41	1.63
tenascin-N precursor [Homo sapiens]	2.07	1.99	1.96	0.99
transforming growth factor beta-1 precursor [Homo sapiens]	0.78	3.79	3.95	0.97
beta-actin-like protein 2 [Homo	0.96	0.09	0.07	0.77

sapiens]				
tropomyosin alpha-1 chain isoform 6 [Homo sapiens]	1.94	0.73	0.63	0.85
4F2 cell-surface antigen heavy chain isoform c [Homo sapiens]	0.82	1.55	1.34	0.87
podocalyxin isoform 1 precursor [Homo sapiens]	2.49	1.19	0.98	0.82
alpha-N-acetylglucosaminidase precursor [Homo sapiens]	6.90	2.32	1.20	0.52
vacuolar protein sorting-associated protein 13C isoform 2A [Homo sapiens]	0.88	1.56	0.32	0.21
vacuolar protein sorting-associated protein 13C isoform 2B [Homo sapiens]	0.88	1.56	0.32	0.21
complement C1r subcomponent precursor [Homo sapiens]	2.07	9.20	6.66	0.72
vacuolar protein sorting-associated protein 13C isoform 1B [Homo sapiens]	0.88	1.56	0.32	0.21
NME1-NME2 protein [Homo sapiens]	1.74	0.32	0.25	0.79
neuropilin-1 isoform c precursor [Homo sapiens]	0.95	3.93	3.77	0.96
histone H2B type 2-F isoform a [Homo sapiens]	3.33	0.13	0.07	0.51
neuropilin-1 isoform b precursor [Homo sapiens]	0.95	3.93	3.77	0.96
tyrosine-protein kinase Mer precursor [Homo sapiens]	1.28	7.33	9.20	1.26
alpha-2-macroglobulin precursor [Homo sapiens]	0.66	2.33	5.11	1.59
proteoglycan 4 isoform A precursor [Homo sapiens]	0.88	2.31	2.20	0.96
complement C4-A isoform 1 preproprotein [Homo sapiens]	2.60	9.32	4.63	0.50
superoxide dismutase [Mn], mitochondrial isoform A precursor [Homo sapiens]	1.37	1.49	0.82	0.55
superoxide dismutase [Mn], mitochondrial isoform B precursor [Homo sapiens]	1.37	1.49	0.82	0.55
complement factor B preproprotein [Homo sapiens]	1.43	8.64	7.11	0.82
actin-related protein 2/3 complex subunit 4 isoform b [Homo sapiens]	0.88	0.13	0.11	0.85
CD166 antigen isoform 1 precursor [Homo sapiens]	1.74	3.51	2.73	0.78
argininosuccinate lyase isoform 2	2.37	0.53	0.42	0.79

[Homo sapiens]				
argininosuccinate lyase isoform 3				
[Homo sapiens]	1.54	1.41	2.71	1.92
liver carboxylesterase 1 isoform c				
precursor [Homo sapiens]	1.69	6.12	1.35	0.22
liver carboxylesterase 1 isoform b				
precursor [Homo sapiens]	1.69	6.12	1.35	0.22
liver carboxylesterase 1 isoform a				
precursor [Homo sapiens]	1.69	6.12	1.35	0.22
inter-alpha-trypsin inhibitor heavy				
chain H2 precursor [Homo sapiens]	1.58	7.16	10.60	1.48
peptidase inhibitor 16 precursor				
[Homo sapiens]	1.58	3.83	4.36	1.14
fibrinogen beta chain isoform 1				
preproprotein [Homo sapiens]	1.71	0.13	0.11	0.85
fibrinogen gamma chain isoform				
gamma-A precursor [Homo sapiens]	1.80	0.10	0.07	0.75
fibrinogen gamma chain isoform				
gamma-B precursor [Homo sapiens]	1.80	0.10	0.07	0.75
glycogen phosphorylase, liver form				
isoform 1 [Homo sapiens]	1.26	0.18	0.13	0.74
cell surface glycoprotein MUC18				
precursor [Homo sapiens]	1.90	3.26	3.37	1.03
phosphoglycerate mutase 4 [Homo				
sapiens]	0.96	0.39	0.32	0.81
myeloblastin precursor [Homo				
sapiens]	2.40	0.57	0.41	0.72
alcohol dehydrogenase 4 [Homo				
sapiens]	1.28	5.12	1.89	0.37
apolipoprotein A-IV precursor [Homo				
sapiens]	1.43	7.74	8.36	1.08
annexin A6 isoform 1 [Homo				
sapiens]	1.71	0.20	0.14	0.74
cysteine-rich with EGF-like domain				
protein 1 isoform 1 precursor [Homo				
sapiens]	1.26	2.49	0.70	0.28
serpin B8 isoform b [Homo sapiens]	2.66	0.37	0.35	0.95
A disintegrin and metalloproteinase				
with thrombospondin motifs 13				
isoform 2 preproprotein [Homo				
sapiens]	2.07	3.41	3.63	1.07
proteasome subunit beta type-8				
isoform E2 proprotein [Homo				
sapiens]	0.89	0.26	0.27	1.02
ubiquitin-conjugating enzyme E2				
variant 1 isoform d [Homo sapiens]	0.84	0.10	0.13	1.33
corticosteroid-binding globulin				
precursor [Homo sapiens]	1.00	3.05	3.69	1.21

heparin cofactor 2 precursor [Homo sapiens]	1.43	7.33	5.97	0.82
plasma protease C1 inhibitor precursor [Homo sapiens]	1.22	8.01	7.80	0.97
serine protease inhibitor Kazal-type 5 isoform b precursor [Homo sapiens]	0.77	0.91	0.81	0.87
plasminogen-like protein B precursor [Homo sapiens]	0.96	4.12	4.16	1.01
matrix metalloproteinase-9 preproprotein [Homo sapiens]	1.34	0.25	0.35	1.43
vascular endothelial growth factor A isoform a [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform b [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform c [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform d [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform e [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform f [Homo sapiens]	1.19	0.26	0.19	0.73
vascular endothelial growth factor A isoform g [Homo sapiens]	1.19	0.26	0.19	0.73
plasma kallikrein preproprotein [Homo sapiens]	1.58	5.99	5.63	0.94
nucleophosmin isoform 3 [Homo sapiens]	1.58	0.42	0.32	0.76
R-spondin-4 isoform 1 precursor [Homo sapiens]	1.82	0.10	0.04	0.44
putative sodium-coupled neutral amino acid transporter 10 isoform a [Homo sapiens]	1.37	6.20	7.63	1.23
EGF-containing fibulin-like extracellular matrix protein 1 precursor [Homo sapiens]	0.99	3.14	4.65	1.48
collagen alpha-1(VI) chain precursor [Homo sapiens]	0.88	1.55	1.37	0.88
complement C1q subcomponent subunit B precursor [Homo sapiens]	0.97	3.55	3.66	1.03
integrin alpha-M isoform 2 precursor [Homo sapiens]	1.00	0.32	0.28	0.89
vasorin precursor [Homo sapiens]	2.07	10.04	7.64	0.76
complement component C1q receptor precursor [Homo sapiens]	0.88	1.57	1.47	0.94
vitronectin precursor [Homo sapiens]	1.28	5.56	3.37	0.61
neutral alpha-glucosidase AB isoform	2.49	0.73	0.51	0.71

3 precursor [Homo sapiens]				
myosin light polypeptide 6 isoform 2 [Homo sapiens]	0.78	0.12	0.12	0.94
collagen alpha-3(IV) chain precursor [Homo sapiens]	1.52	8.57	17.16	2.00
integrin beta-2 precursor [Homo sapiens]	0.89	0.37	0.32	0.86
von Willebrand factor preproprotein [Homo sapiens]	2.24	3.68	3.81	1.03
phosphate-regulating neutral endopeptidase isoform 1 [Homo sapiens]	0.88	9.08	9.85	1.08
R-spondin-4 isoform 2 precursor [Homo sapiens]	1.82	0.10	0.04	0.44
osteopontin isoform OPN-a precursor [Homo sapiens]	2.60	2.15	2.00	0.93
osteopontin isoform OPN-c precursor [Homo sapiens]	2.60	2.15	2.00	0.93
ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform 1 preproprotein [Homo sapiens]	1.27	2.06	3.70	1.80
ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform 2 preproprotein [Homo sapiens]	1.27	2.06	3.70	1.80
myosin-11 isoform SM2B [Homo sapiens]	1.28	0.14	0.15	1.05
myosin-11 isoform SM1B [Homo sapiens]	1.28	0.14	0.15	1.05
ly6/PLAUR domain-containing protein 3 precursor [Homo sapiens]	0.95	0.71	0.50	0.70
neural cell adhesion molecule 1 isoform 1 precursor [Homo sapiens]	0.99	3.27	3.52	1.08
hydroxyacylglutathione hydrolase, mitochondrial isoform 2 [Homo sapiens]	0.84	0.63	0.69	1.08
hydroxyacylglutathione hydrolase, mitochondrial isoform 1 precursor [Homo sapiens]	0.84	0.63	0.69	1.08
gastrokine-1 [Homo sapiens]	0.97	3.40	3.69	1.08
vascular endothelial growth factor receptor 3 isoform 2 precursor [Homo sapiens]	0.88	4.71	3.80	0.81
vascular endothelial growth factor receptor 3 isoform 1 precursor [Homo sapiens]	0.88	4.71	3.80	0.81
receptor-type tyrosine-protein	0.65	1.24	1.23	0.94

phosphatase S isoform 1 precursor [Homo sapiens]				
receptor-type tyrosine-protein phosphatase S isoform 3 precursor [Homo sapiens]	0.65	3.27	2.71	0.83
receptor-type tyrosine-protein phosphatase S isoform 2 precursor [Homo sapiens]	0.65	1.24	1.23	0.94
receptor-type tyrosine-protein phosphatase S isoform 4 precursor [Homo sapiens]	0.65	3.27	2.71	0.83
filamin-B isoform 2 [Homo sapiens]	0.84	0.41	0.52	1.27
apolipoprotein B-100 precursor [Homo sapiens]	1.74	3.59	4.55	1.27
coagulation factor V precursor [Homo sapiens]	2.60	5.94	7.87	1.32
neurofilament light polypeptide [Homo sapiens]	1.00	0.35	0.44	1.26
histone H2A type 2-A [Homo sapiens]	3.93	0.91	0.37	0.40
glucose-6-phosphate 1- dehydrogenase isoform b [Homo sapiens]	0.97	0.11	0.15	1.41
insulin-like growth factor II isoform 1 preproprotein [Homo sapiens]	0.73	4.64	2.65	0.65
keratin, type II cytoskeletal 3 [Homo sapiens]	0.68	0.11	0.11	0.94
glucose-6-phosphate 1- dehydrogenase isoform a [Homo sapiens]	0.97	0.11	0.15	1.41
receptor-type tyrosine-protein phosphatase F isoform 2 precursor [Homo sapiens]	0.96	1.09	1.47	1.36
receptor-type tyrosine-protein phosphatase F isoform 1 precursor [Homo sapiens]	0.96	1.09	1.47	1.36
calpastatin isoform f [Homo sapiens]	0.58	0.26	0.24	0.88
prosaposin isoform b preproprotein [Homo sapiens]	1.77	0.29	0.35	1.22
prosaposin isoform c preproprotein [Homo sapiens]	1.77	0.29	0.35	1.22
phospholipase B-like 1 precursor [Homo sapiens]	0.57	0.04	0.05	1.18
myc-associated zinc finger protein isoform 2 [Homo sapiens]	0.83	1.90	1.98	1.04
myc-associated zinc finger protein isoform 1 [Homo sapiens]	0.83	1.90	1.98	1.04
collagen alpha-1(I) chain	0.45	0.23	0.21	0.90

preproprotein [Homo sapiens]				
collagen alpha-1(XVIII) chain isoform 2 precursor [Homo sapiens]	2.07	2.88	3.78	1.31
collagen alpha-1(XVIII) chain isoform 1 precursor [Homo sapiens]	2.07	2.88	3.78	1.31
coagulation factor XIII B chain precursor [Homo sapiens]	0.77	1.12	1.65	1.22
cadherin-related family member 5 isoform 1 precursor [Homo sapiens]	2.07	3.24	4.80	1.48
cadherin-related family member 5 isoform 3 precursor [Homo sapiens]	2.07	3.24	4.80	1.48
lysosome-associated membrane glycoprotein 1 precursor [Homo sapiens]	1.74	2.39	2.27	0.95
spectrin beta chain, non-erythrocytic 1 isoform 1 [Homo sapiens]	2.24	3.52	2.53	0.72
spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	2.24	3.52	2.53	0.72
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	0.92	0.29	0.21	0.71
tropomyosin alpha-3 chain isoform 1 [Homo sapiens]	1.24	0.20	0.20	1.02
tropomyosin alpha-3 chain isoform 4 [Homo sapiens]	1.47	0.21	0.20	0.97
tropomyosin alpha-3 chain isoform 3 [Homo sapiens]	1.35	0.21	0.20	0.97
tropomyosin alpha-3 chain isoform 5 [Homo sapiens]	1.47	0.21	0.20	0.97
protein S100-A7 [Homo sapiens]	1.43	0.04	0.75	20.09
nidogen-1 precursor [Homo sapiens]	1.00	6.89	6.39	0.93
complement C3 precursor [Homo sapiens]	0.79	0.16	0.15	0.92
galectin-3 isoform 1 [Homo sapiens]	0.76	1.21	1.28	0.98
spectrin beta chain, non-erythrocytic 4 isoform sigma1 [Homo sapiens]	0.88	0.28	0.21	0.75
collagen alpha-2(VI) chain isoform 2C2 precursor [Homo sapiens]	1.74	3.57	3.44	0.96
neural cell adhesion molecule 1 isoform 3 precursor [Homo sapiens]	0.99	3.27	3.52	1.08
neural cell adhesion molecule 1 isoform 2 precursor [Homo sapiens]	0.99	3.27	3.52	1.08
filamin-A isoform 1 [Homo sapiens]	1.28	0.44	0.52	1.19
extracellular serine/threonine protein kinase FAM20C precursor [Homo sapiens]	2.60	2.24	2.09	0.93
apolipoprotein(a) precursor [Homo sapiens]	0.68	5.13	0.84	0.28
dopamine beta-hydroxylase	1.58	3.67	4.58	1.25

precursor [Homo sapiens]				
diphthamide biosynthesis protein 1 [Homo sapiens]	1.50	11.83	11.97	1.01
alkaline phosphatase, tissue-nonspecific isozyme isoform 1 precursor [Homo sapiens]	0.76	2.14	1.39	0.78
cysteine-rich with EGF-like domain protein 1 isoform 2 precursor [Homo sapiens]	1.26	2.49	0.70	0.28
filamin-C isoform a [Homo sapiens]	0.84	0.41	0.52	1.27
phosphatidylethanolamine-binding protein 4 precursor [Homo sapiens]	0.66	4.76	2.53	0.62
complement factor H-related protein 4 isoform 3 precursor [Homo sapiens]	0.76	3.93	5.19	1.14
lactoylglutathione lyase [Homo sapiens]	0.73	0.34	0.32	0.97
complement factor H-related protein 1 precursor [Homo sapiens]	2.60	4.64	3.20	0.69
extracellular superoxide dismutase [Cu-Zn] precursor [Homo sapiens]	0.91	1.71	5.49	3.22
dmX-like protein 2 isoform 2 [Homo sapiens]	0.93	9.72	12.08	1.24
tissue alpha-L-fucosidase precursor [Homo sapiens]	1.54	1.50	0.71	0.48
coagulation factor XIII A chain precursor [Homo sapiens]	0.83	0.35	0.30	0.87
lysosomal protective protein isoform a precursor [Homo sapiens]	0.97	2.38	1.82	0.77
keratin, type II cytoskeletal 1 [Homo sapiens]	0.24	0.42	0.39	0.89
laminin subunit alpha-2 isoform b precursor [Homo sapiens]	0.70	4.20	3.24	0.79
keratin, type II cytoskeletal 6B [Homo sapiens]	0.73	0.14	0.11	0.84
cation-independent mannose-6-phosphate receptor precursor [Homo sapiens]	2.60	2.14	2.00	0.93
acyl-CoA-binding protein isoform 3 [Homo sapiens]	1.38	0.35	0.29	0.81
acyl-CoA-binding protein isoform 2 [Homo sapiens]	1.38	0.35	0.29	0.81
mastermind-like domain-containing protein 1 isoform 2 [Homo sapiens]	0.78	0.36	0.35	0.92
serpin A11 precursor [Homo sapiens]	0.96	5.23	5.65	1.08
protein-arginine deiminase type-2 [Homo sapiens]	0.74	0.05	0.04	0.78
BRO1 domain-containing protein	0.81	0.08	0.81	4.45

BROX isoform a [Homo sapiens]				
neutrophil defensin 1 precursor [Homo sapiens]	1.41	0.11	0.10	0.92
kinesin-like protein KIF26B [Homo sapiens]	2.59	0.64	0.68	1.07
proliferation-associated protein 2G4 [Homo sapiens]	1.18	0.40	0.14	0.34
prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]	1.00	1.88	2.37	1.26
basement membrane-specific heparan sulfate proteoglycan core protein isoform b precursor [Homo sapiens]	0.95	2.98	3.19	1.07
low affinity immunoglobulin gamma Fc region receptor II-c precursor [Homo sapiens]	0.77	1.80	0.67	0.49
dual oxidase 2 precursor [Homo sapiens]	0.73	0.30	0.29	0.92
low affinity immunoglobulin gamma Fc region receptor III-B isoform 2 precursor [Homo sapiens]	2.11	1.39	3.11	2.24
testis-expressed sequence 15 protein [Homo sapiens]	1.94	3.76	3.84	1.02
phosphoglucomutase-like protein 5 [Homo sapiens]	1.35	0.47	2.73	5.76
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapiens]	2.24	6.37	8.82	1.38
POTE ankyrin domain family member E [Homo sapiens]	0.88	0.16	0.15	0.94
chitinase-3-like protein 1 precursor [Homo sapiens]	2.24	0.61	0.64	1.05
coagulation factor XII precursor [Homo sapiens]	1.74	5.44	5.93	1.09
laminin subunit gamma-1 precursor [Homo sapiens]	0.93	0.87	0.80	0.92
schlafen family member 5 [Homo sapiens]	1.27	1.09	2.47	2.26
multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [Homo sapiens]	1.90	5.11	7.95	1.56
mast/stem cell growth factor receptor Kit isoform 2 precursor [Homo sapiens]	1.41	2.82	2.00	0.71
selenoprotein P isoform 1 precursor [Homo sapiens]	0.97	5.98	6.73	1.13
selenoprotein P isoform 2 [Homo sapiens]	0.97	5.98	6.73	1.13

sapiens]				
probable E3 ubiquitin-protein ligase TRIM8 [Homo sapiens]	0.76	0.64	0.88	1.16
cell adhesion molecule 1 isoform 1 precursor [Homo sapiens]	0.99	0.20	0.19	0.96
cell adhesion molecule 1 isoform 2 precursor [Homo sapiens]	0.99	0.20	0.19	0.96
probable G-protein coupled receptor 116 precursor [Homo sapiens]	1.35	13.00	9.94	0.76
ubiquitin carboxyl-terminal hydrolase 5 isoform 2 [Homo sapiens]	1.18	0.19	0.11	0.58
ubiquitin carboxyl-terminal hydrolase 5 isoform 1 [Homo sapiens]	1.18	0.19	0.11	0.58
receptor-type tyrosine-protein phosphatase eta isoform 2 precursor [Homo sapiens]	2.60	4.01	4.25	1.06
receptor-type tyrosine-protein phosphatase eta isoform 1 precursor [Homo sapiens]	2.60	4.01	4.25	1.06
sialic acid-binding Ig-like lectin 14 precursor [Homo sapiens]	0.93	2.97	2.45	0.83
xaa-Pro dipeptidase isoform 1 [Homo sapiens]	0.88	1.39	1.55	1.11
thioredoxin-related transmembrane protein 1 precursor [Homo sapiens]	3.62	0.07	0.65	9.54
prothymosin alpha isoform 2 [Homo sapiens]	0.74	0.91	0.70	0.79
prothymosin alpha isoform 1 [Homo sapiens]	0.74	0.91	0.70	0.79
myristoylated alanine-rich C-kinase substrate [Homo sapiens]	0.70	0.11	0.16	1.25
intercellular adhesion molecule 2 precursor [Homo sapiens]	0.95	3.68	4.63	1.26
beta-2-glycoprotein 1 precursor [Homo sapiens]	2.24	8.71	7.85	0.90
keratin, type II cytoskeletal 75 [Homo sapiens]	0.73	0.17	0.12	0.76
POTE ankyrin domain family member F [Homo sapiens]	0.91	0.18	0.18	0.99
protein HEG homolog 1 precursor [Homo sapiens]	0.88	7.77	10.12	1.30
heat shock protein HSP 90-alpha isoform 1 [Homo sapiens]	0.82	0.13	0.15	1.22
tenascin precursor [Homo sapiens]	0.83	1.23	1.56	1.26
dedicator of cytokinesis protein 10 DOCK10.1 [Homo sapiens]	1.74	41.25	57.82	1.40

heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	0.82	0.13	0.15	1.22
IgGFC-binding protein precursor [Homo sapiens]	0.96	3.24	2.38	0.74
V-set and immunoglobulin domain-containing protein 4 isoform 2 precursor [Homo sapiens]	0.67	0.41	0.67	1.30
spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	1.28	0.60	0.46	0.77
taste receptor type 2 member 20 [Homo sapiens]	0.82	0.45	0.09	0.32
keratin, type II cytoskeletal 6C [Homo sapiens]	0.73	0.14	0.11	0.84
inter-alpha-trypsin inhibitor heavy chain H1 isoform a precursor [Homo sapiens]	1.28	5.69	6.51	1.15
kininogen-1 isoform 1 precursor [Homo sapiens]	1.21	19.55	19.02	0.97
alpha-2-HS-glycoprotein preproprotein [Homo sapiens]	1.58	10.80	9.53	0.88
N-acetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	0.95	6.04	5.62	0.93
tetranectin precursor [Homo sapiens]	0.99	7.87	4.41	0.56
proteasome subunit alpha type-4 isoform 2 [Homo sapiens]	0.88	0.76	0.77	1.02
purine nucleoside phosphorylase [Homo sapiens]	0.91	0.13	0.11	0.86
bactericidal permeability-increasing protein precursor [Homo sapiens]	2.70	0.22	0.18	0.83
neogenin isoform 1 precursor [Homo sapiens]	1.35	4.14	4.58	1.11
heterogeneous nuclear ribonucleoprotein M isoform b [Homo sapiens]	0.92	0.85	0.46	0.54
laminin subunit gamma-2 isoform a precursor [Homo sapiens]	2.21	0.13	0.07	0.55
laminin subunit gamma-2 isoform b precursor [Homo sapiens]	2.21	0.13	0.07	0.55
receptor-type tyrosine-protein phosphatase mu isoform 2 precursor [Homo sapiens]	0.95	0.62	0.74	1.18
receptor-type tyrosine-protein phosphatase mu isoform 1 precursor [Homo sapiens]	0.95	0.62	0.74	1.18
procollagen C-endopeptidase enhancer 1 precursor [Homo sapiens]	0.71	2.27	2.18	0.92

sapiens]				
neurofilament medium polypeptide isoform 2 [Homo sapiens]	1.00	0.35	0.44	1.26
neurofilament medium polypeptide isoform 1 [Homo sapiens]	1.00	0.35	0.44	1.26
receptor-type tyrosine-protein phosphatase beta isoform b precursor [Homo sapiens]	0.88	1.12	1.18	1.06
receptor-type tyrosine-protein phosphatase beta isoform a [Homo sapiens]	0.88	1.12	1.18	1.06
filamin-A isoform 2 [Homo sapiens]	1.28	0.44	0.52	1.19
ezrin [Homo sapiens]	0.83	0.39	0.25	0.63
pregnancy zone protein precursor [Homo sapiens]	0.97	1.19	2.78	2.33
insulin-like growth factor I isoform 1 preproprotein [Homo sapiens]	1.28	7.34	8.34	1.14
insulin-like growth factor I isoform 2 preproprotein [Homo sapiens]	1.28	7.34	8.34	1.14
insulin-like growth factor I isoform 3 preproprotein [Homo sapiens]	1.28	7.34	8.34	1.14
cyclin-dependent kinase-like 3 isoform 2 [Homo sapiens]	0.83	3.93	3.84	0.98
cyclin-dependent kinase-like 3 isoform 1 [Homo sapiens]	0.83	3.93	3.84	0.98
complement component C8 gamma chain precursor [Homo sapiens]	2.49	6.11	7.57	1.24
cadherin-5 preproprotein [Homo sapiens]	0.93	2.91	2.06	0.71
prenylcysteine oxidase 1 precursor [Homo sapiens]	0.91	0.87	1.19	1.36
heat shock 70 kDa protein 1A/1B [Homo sapiens]	2.07	0.15	0.12	0.81
intercellular adhesion molecule 1 precursor [Homo sapiens]	0.89	2.49	2.76	1.11
intercellular adhesion molecule 3 precursor [Homo sapiens]	1.50	1.45	1.41	0.97
laminin subunit beta-1 precursor [Homo sapiens]	0.99	2.98	3.62	1.21
plastin-2 [Homo sapiens]	1.27	0.34	0.31	0.90
alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase [Homo sapiens]	0.93	1.85	1.77	0.96
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	1.28	5.04	6.69	1.33
ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2 precursor [Homo sapiens]	1.72	3.32	2.58	0.78

sapiens]				
endoglin isoform 1 precursor [Homo sapiens]	0.93	2.14	1.95	0.91
tumor protein 63 isoform 2 [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein 63 isoform 3 [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein 63 isoform 4 [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein 63 isoform 5 [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein 63 isoform 6 [Homo sapiens]	0.56	0.30	0.11	0.50
cholesterol ester transfer protein isoform 1 precursor [Homo sapiens]	1.27	7.24	3.32	0.46
rab GDP dissociation inhibitor beta isoform 2 [Homo sapiens]	0.96	0.20	0.16	0.79
lysosome-associated membrane glycoprotein 2 isoform C precursor [Homo sapiens]	1.60	1.88	2.37	1.26
trypsin-3 isoform 1 preproprotein [Homo sapiens]	0.76	0.63	0.62	0.93
drebrin-like protein isoform c [Homo sapiens]	0.88	0.50	0.51	1.02
peptidyl-prolyl cis-trans isomerase A-like 4G [Homo sapiens]	1.74	0.17	0.12	0.74
complement C4-B preproprotein [Homo sapiens]	0.88	4.43	3.43	0.77
neuropilin-1 isoform a precursor [Homo sapiens]	0.95	3.93	3.77	0.96
protein DJ-1 [Homo sapiens]	0.97	0.25	0.20	0.78
haptoglobin isoform 2 preproprotein [Homo sapiens]	0.89	0.78	0.15	0.19
hepatoma-derived growth factor isoform b [Homo sapiens]	1.55	0.04	0.70	16.64
hepatoma-derived growth factor isoform c [Homo sapiens]	1.55	0.04	0.70	16.64
tumor protein p73 isoform b [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform c [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform d [Homo sapiens]	0.56	0.30	0.11	0.50
serum amyloid A-2 protein isoform a precursor [Homo sapiens]	1.43	0.87	1.41	1.61
tenascin-X isoform 1 precursor [Homo sapiens]	0.95	2.83	4.65	1.65
histone H3.3C [Homo sapiens]	2.73	0.32	0.21	0.65

syntaxin-binding protein 2 isoform a [Homo sapiens]	1.26	0.06	0.05	0.83
syntaxin-binding protein 2 isoform b [Homo sapiens]	1.26	0.06	0.05	0.83
filamin-C isoform b [Homo sapiens]	0.84	0.41	0.52	1.27
hepatocyte growth factor receptor isoform a precursor [Homo sapiens]	1.28	1.17	2.08	1.78
acid ceramidase isoform b [Homo sapiens]	2.46	0.48	0.46	0.96
acid ceramidase isoform a preproprotein [Homo sapiens]	2.46	0.48	0.46	0.96
acid ceramidase isoform c [Homo sapiens]	2.46	0.48	0.46	0.96
gelsolin isoform b [Homo sapiens]	0.99	6.68	6.72	1.00
low affinity immunoglobulin gamma Fc region receptor III-A isoform b precursor [Homo sapiens]	2.19	3.58	5.49	1.53
low affinity immunoglobulin gamma Fc region receptor III-A isoform c precursor [Homo sapiens]	2.19	3.58	5.49	1.53
low affinity immunoglobulin gamma Fc region receptor III-A isoform d precursor [Homo sapiens]	2.19	3.58	5.49	1.53
insulin-like growth factor II isoform 2 [Homo sapiens]	0.73	4.64	2.65	0.65
delta-aminolevulinic acid dehydratase [Homo sapiens]	0.56	0.13	0.10	0.80
platelet-activating factor acetylhydrolase precursor [Homo sapiens]	1.46	0.89	2.55	2.88
lysosomal protective protein isoform b precursor [Homo sapiens]	0.97	2.38	1.82	0.77
serine protease inhibitor Kazal-type 5 isoform a precursor [Homo sapiens]	0.77	0.91	0.81	0.87
serine protease inhibitor Kazal-type 5 isoform c precursor [Homo sapiens]	0.77	0.91	0.81	0.87
proteoglycan 4 isoform B precursor [Homo sapiens]	0.88	2.31	2.20	0.96
proteoglycan 4 isoform C precursor [Homo sapiens]	0.88	2.31	2.20	0.96
proteoglycan 4 isoform D precursor [Homo sapiens]	0.88	2.31	2.20	0.96
72 kDa type IV collagenase isoform b [Homo sapiens]	0.50	1.49	1.30	0.86
complement component C6 precursor [Homo sapiens]	1.43	6.22	6.21	1.00

1,4-alpha-glucan-branching enzyme [Homo sapiens]	0.91	0.41	0.35	0.85
SPARC-like protein 1 isoform 1 precursor [Homo sapiens]	2.79	11.02	12.13	1.10
ATPase SWSAP1 [Homo sapiens]	0.81	0.73		
carbonic anhydrase 1 isoform a [Homo sapiens]	0.83	0.17	0.13	0.74
vitamin K-dependent protein S preproprotein [Homo sapiens]	1.90	5.42	5.90	1.09
serrate RNA effector molecule homolog isoform c [Homo sapiens]	1.74	2.91	2.80	0.96
serrate RNA effector molecule homolog isoform d [Homo sapiens]	1.74	2.91	2.80	0.96
serrate RNA effector molecule homolog isoform e [Homo sapiens]	1.74	2.91	2.80	0.96
plasma serine protease inhibitor preproprotein [Homo sapiens]	1.43	7.07	4.88	0.69
hexokinase-3 [Homo sapiens]	0.92	0.19	0.15	0.78
alpha-actinin-1 isoform a [Homo sapiens]	0.79	0.30	0.24	0.83
alpha-actinin-1 isoform c [Homo sapiens]	0.79	0.30	0.24	0.83
Golgin subfamily A member 2 [Homo sapiens]	4.25	1.51	1.20	0.80
receptor-type tyrosine-protein phosphatase gamma [Homo sapiens]	0.99	5.98	6.82	1.14
spectrin alpha chain, non- erythrocytic 1 isoform 1 [Homo sapiens]	1.28	0.60	0.46	0.77
high mobility group protein B2 [Homo sapiens]	1.38	0.07	0.08	1.22
proteasome subunit beta type-5 isoform 2 [Homo sapiens]	0.88	0.56	0.49	0.87
ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform 3 preproprotein [Homo sapiens]	1.27	2.06	3.70	1.80
keratin, type I cytoskeletal 10 [Homo sapiens]	0.40	0.29	0.41	1.28
hypoxia up-regulated protein 1 precursor [Homo sapiens]	1.27	3.76	3.84	1.02
glial fibrillary acidic protein isoform 2 [Homo sapiens]	2.07	0.13	0.07	0.56
pre-mRNA 3'-end-processing factor FIP1 isoform 2 [Homo sapiens]	3.12	0.26	0.22	0.86
pre-mRNA 3'-end-processing factor FIP1 isoform 3 [Homo sapiens]	3.12	0.26	0.22	0.86
hepatocyte growth factor-like	1.28	4.43	4.23	0.95

protein precursor [Homo sapiens]				
thyroxine-binding globulin precursor [Homo sapiens]	1.46	10.14	9.80	0.97
L-lactate dehydrogenase A chain isoform 2 [Homo sapiens]	1.40	0.13	0.08	0.62
ubiquitin-40S ribosomal protein S27a precursor [Homo sapiens]	1.74	0.34	0.39	1.15
poliovirus receptor isoform beta precursor [Homo sapiens]	1.18	7.34	8.79	1.20
poliovirus receptor isoform gamma precursor [Homo sapiens]	1.18	7.34	8.79	1.20
annexin A2 isoform 2 [Homo sapiens]	1.74	0.19	0.20	1.03
amyloid beta A4 protein isoform d [Homo sapiens]	0.99	6.19	3.99	0.65
plastin-3 isoform 1 [Homo sapiens]	1.19	0.28	0.19	0.68
DEP domain-containing protein 5 isoform 3 [Homo sapiens]	1.43	0.77	1.44	1.88
putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform 1 [Homo sapiens]	0.96	0.31	0.32	1.04
periostin isoform 1 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
periostin isoform 2 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
periostin isoform 3 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
periostin isoform 4 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
amyloid beta A4 protein isoform e precursor [Homo sapiens]	0.99	3.59	3.36	0.94
amyloid beta A4 protein isoform f precursor [Homo sapiens]	0.99	6.19	3.99	0.65
amyloid beta A4 protein isoform g [Homo sapiens]	0.99	3.59	3.36	0.94
protein RCC2 [Homo sapiens]	0.95	0.91	0.50	0.55
low affinity immunoglobulin gamma Fc region receptor II-a isoform 1 precursor [Homo sapiens]	0.81	1.41	1.51	0.99
glia-derived nexin isoform b precursor [Homo sapiens]	0.79	2.30	2.61	1.29
glia-derived nexin isoform c precursor [Homo sapiens]	0.79	2.30	2.61	1.29
apolipoprotein L1 isoform c [Homo sapiens]	0.62	0.68	0.56	0.84
amyloid-like protein 2 isoform 2 precursor [Homo sapiens]	2.49	9.52	5.88	0.62
amyloid-like protein 2 isoform 3 precursor [Homo sapiens]	2.49	9.52	5.88	0.62

amyloid-like protein 2 isoform 4 precursor [Homo sapiens]	2.49	9.52	5.88	0.62
putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform 3 [Homo sapiens]	0.96	0.31	0.32	1.04
cysteine-rich secretory protein 2 precursor [Homo sapiens]	1.40	12.27	17.13	1.40
protein-arginine deiminase type-4 [Homo sapiens]	1.89	0.46	0.44	0.96
activated RNA polymerase II transcriptional coactivator p15 [Homo sapiens]	1.29	0.62	2.74	4.39
eukaryotic translation initiation factor 5A-1 isoform A [Homo sapiens]	0.99	0.26	0.23	0.88
peptidyl-prolyl cis-trans isomerase A-like 4A/B/C [Homo sapiens]	1.58	0.28	0.21	0.75
secretogranin-1 precursor [Homo sapiens]	1.50	3.39	2.78	0.82
extracellular matrix protein 1 isoform 1 precursor [Homo sapiens]	0.84	4.21	3.09	0.73
extracellular matrix protein 1 isoform 2 precursor [Homo sapiens]	0.92	3.32	2.36	0.71
multimerin-2 precursor [Homo sapiens]	0.97	9.52	6.89	0.72
proteasome subunit alpha type-1 isoform 3 [Homo sapiens]	0.76	1.31	2.39	1.42
WD repeat-containing protein 91 [Homo sapiens]	0.88	2.94	4.65	1.58
proteasome subunit beta type-5 isoform 3 [Homo sapiens]	0.71	0.28	0.32	1.44
myosin regulatory light chain 12B [Homo sapiens]	0.82	0.15	0.19	1.29
soluble scavenger receptor cysteine-rich domain-containing protein SSC5D isoform 1 precursor [Homo sapiens]	0.62	0.71	0.70	0.93
SHC-transforming protein 4 [Homo sapiens]	1.43	20.57	13.57	0.66
talin-1 [Homo sapiens]	1.38	0.27	0.39	1.41
calmodulin-like protein 5 [Homo sapiens]	0.35	0.35	0.21	0.68
tropomyosin alpha-4 chain isoform 1 [Homo sapiens]	1.90	0.60	0.54	0.90
proline-rich acidic protein 1 isoform 2 precursor [Homo sapiens]	0.96	3.95	3.69	0.94
proline-rich acidic protein 1 isoform 1 precursor [Homo sapiens]	0.96	3.95	3.69	0.94
pantetheinase precursor [Homo sapiens]	2.79	3.58	5.05	1.41

sapiens]				
aldehyde dehydrogenase family 16 member A1 isoform 1 [Homo sapiens]	0.82	2.54	4.85	1.45
aldehyde dehydrogenase family 16 member A1 isoform 2 [Homo sapiens]	0.82	2.54	4.85	1.45
stathmin isoform b [Homo sapiens]	0.83	0.18	0.13	0.74
Golgi apparatus protein 1 isoform 2 precursor [Homo sapiens]	1.35	13.31	9.67	0.73
Golgi apparatus protein 1 isoform 3 precursor [Homo sapiens]	1.35	13.31	9.67	0.73
integrin alpha-M isoform 1 precursor [Homo sapiens]	1.00	0.32	0.28	0.89
interstitial collagenase isoform 2 [Homo sapiens]	0.88	0.15	0.11	0.79
platelet-activating factor acetylhydrolase IB subunit gamma [Homo sapiens]	1.74	0.37	0.23	0.61
complement C2 isoform 2 precursor [Homo sapiens]	1.90	4.28	5.53	1.29
insulin-like growth factor-binding protein complex acid labile subunit isoform 1 precursor [Homo sapiens]	0.97	4.18	4.53	1.08
keratin, type II cytoskeletal 72 isoform 2 [Homo sapiens]	0.73	0.17	0.12	0.76
sex hormone-binding globulin isoform 4 precursor [Homo sapiens]	2.07	3.59	4.68	1.30
sex hormone-binding globulin isoform 2 precursor [Homo sapiens]	0.96	3.37	4.14	1.23
sex hormone-binding globulin isoform 3 precursor [Homo sapiens]	1.74	4.43	4.07	0.92
triosephosphate isomerase isoform 2 [Homo sapiens]	1.27	0.16	0.12	0.74
CD109 antigen isoform 2 preproprotein [Homo sapiens]	0.92	0.25	0.21	0.87
CD109 antigen isoform 3 preproprotein [Homo sapiens]	0.92	0.25	0.21	0.87
endomucin isoform 2 precursor [Homo sapiens]	1.31	10.71	15.71	1.47
histone H2B type 2-F isoform b [Homo sapiens]	3.33	0.13	0.07	0.51
glycogen [starch] synthase, muscle isoform 2 [Homo sapiens]	1.31	0.04	0.65	16.31
collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]	0.79	2.59	1.51	0.66
collagen alpha-3(VI) chain isoform 3 precursor [Homo sapiens]	0.96	2.59	1.20	0.46

collagen alpha-3(VI) chain isoform 2 precursor [Homo sapiens]	0.96	2.59	1.20	0.46
glycogen phosphorylase, liver form isoform 2 [Homo sapiens]	1.26	0.18	0.13	0.74
perilipin-3 isoform 1 [Homo sapiens]	0.71	0.29	0.29	0.95
perilipin-3 isoform 2 [Homo sapiens]	0.71	0.29	0.29	0.95
perilipin-3 isoform 3 [Homo sapiens]	0.71	0.29	0.29	0.95
peptidyl-prolyl cis-trans isomerase A-like 4D [Homo sapiens]	1.74	0.17	0.12	0.74
filamin-B isoform 1 [Homo sapiens]	0.84	0.41	0.52	1.27
filamin-B isoform 3 [Homo sapiens]	0.84	0.41	0.52	1.27
filamin-B isoform 4 [Homo sapiens]	0.84	0.41	0.52	1.27
glycogen phosphorylase, muscle form isoform 2 [Homo sapiens]	1.24	0.52	0.51	0.97
alpha-2-antiplasmin isoform a precursor [Homo sapiens]	2.24	6.75	6.22	0.92
alpha-2-antiplasmin isoform b precursor [Homo sapiens]	2.07	7.05	6.77	0.96
L-lactate dehydrogenase A chain isoform 3 [Homo sapiens]	1.28	0.22	0.12	0.54
L-lactate dehydrogenase A chain isoform 4 [Homo sapiens]	1.28	0.16	0.12	0.76
L-lactate dehydrogenase A chain isoform 5 [Homo sapiens]	1.28	0.16	0.12	0.76
suprabasin isoform 1 precursor [Homo sapiens]	0.49	1.78	0.84	0.57
suprabasin isoform 3 precursor [Homo sapiens]	0.48	0.29	0.35	1.65
xaa-Pro dipeptidase isoform 2 [Homo sapiens]	0.88	1.39	1.55	1.11
xaa-Pro dipeptidase isoform 3 [Homo sapiens]	0.88	1.39	1.55	1.11
latent-transforming growth factor beta-binding protein 1 isoform LTBP-1L precursor [Homo sapiens]	1.43	3.23	2.27	0.70
latent-transforming growth factor beta-binding protein 1 isoform LTBP-1S precursor [Homo sapiens]	1.43	3.23	2.27	0.70
latent-transforming growth factor beta-binding protein 1 isoform 4 precursor [Homo sapiens]	1.43	3.23	2.27	0.70
latent-transforming growth factor beta-binding protein 1 isoform 3 precursor [Homo sapiens]	1.28	1.78	1.59	0.89
latent-transforming growth factor beta-binding protein 1 isoform 5 precursor [Homo sapiens]	1.28	1.78	1.59	0.89

inter-alpha-trypsin inhibitor heavy chain H1 isoform b [Homo sapiens]	1.28	5.42	6.35	1.17
inter-alpha-trypsin inhibitor heavy chain H1 isoform c [Homo sapiens]	1.90	6.12	6.83	1.11
inter-alpha-trypsin inhibitor heavy chain H4 isoform 2 precursor [Homo sapiens]	2.53	16.58	19.23	1.16
kininogen-1 isoform 3 precursor [Homo sapiens]	1.28	16.49	12.06	0.73
gastricsin isoform 2 preproprotein [Homo sapiens]	0.91	1.90	3.29	1.73
L-selectin precursor [Homo sapiens]	1.00	4.52	4.98	1.10
complement factor H-related protein 3 isoform 2 precursor [Homo sapiens]	0.88	3.51	2.67	0.76
cystatin-F precursor [Homo sapiens]	0.62	0.09	0.15	1.40
lysosomal protective protein isoform c precursor [Homo sapiens]	0.97	2.38	1.82	0.77
protein phosphatase 1 regulatory subunit 12B isoform a [Homo sapiens]	1.52	3.03	3.12	1.03
protein phosphatase 1 regulatory subunit 12B isoform e [Homo sapiens]	1.52	3.03	3.12	1.03
protein phosphatase 1 regulatory subunit 12B isoform f [Homo sapiens]	1.52	3.03	3.12	1.03
interleukin-1 receptor accessory protein isoform 1 precursor [Homo sapiens]	1.58	3.57	7.37	2.06
interleukin-1 receptor accessory protein isoform 2 precursor [Homo sapiens]	1.58	3.57	7.37	2.06
interleukin-1 receptor accessory protein isoform 3 precursor [Homo sapiens]	1.58	3.57	7.37	2.06
plasminogen isoform 2 precursor [Homo sapiens]	0.95	4.21	4.35	1.03
oncostatin-M-specific receptor subunit beta isoform 2 precursor [Homo sapiens]	0.81	0.69	0.80	1.48
uncharacterized protein C10orf62 [Homo sapiens]	0.67	0.55	0.44	0.85
vascular endothelial growth factor A isoform h [Homo sapiens]	1.19	0.26	0.19	0.73
cadherin-related family member 5 isoform 4 precursor [Homo sapiens]	2.07	3.24	4.80	1.48
cadherin-related family member 2	0.96	1.31	0.96	0.73

precursor [Homo sapiens]				
N(4)-(beta-N-acetylglucosaminy)-L-asparaginase isoform 1				
preproprotein [Homo sapiens]	1.47	3.65	3.36	0.92
N(4)-(beta-N-acetylglucosaminy)-L-asparaginase isoform 2				
preproprotein [Homo sapiens]	1.47	3.65	3.36	0.92
4-hydroxyphenylpyruvate dioxygenase isoform 2 [Homo sapiens]	1.28	1.88	1.58	0.84
tubulin alpha chain-like 3 isoform 2 [Homo sapiens]	0.77	0.04	0.70	6.92
plastin-1 [Homo sapiens]	2.60	0.11	0.08	0.73
plastin-3 isoform 2 [Homo sapiens]	1.19	0.28	0.19	0.68
leukocyte immunoglobulin-like receptor subfamily A member 3 isoform 1 precursor [Homo sapiens]	0.62	0.91	0.68	0.78
leukocyte immunoglobulin-like receptor subfamily A member 3 isoform 2 precursor [Homo sapiens]	0.62	0.91	0.68	0.78
complement C1r subcomponent-like protein isoform 1 precursor [Homo sapiens]	1.00	9.59	10.57	1.10
zinc finger protein 548 isoform 2 [Homo sapiens]	1.82	0.08	0.07	0.82
zinc finger protein 548 isoform 1 [Homo sapiens]	1.82	0.08	0.07	0.82
neogenin isoform 3 precursor [Homo sapiens]	1.35	4.14	4.58	1.11
neogenin isoform 2 precursor [Homo sapiens]	1.35	4.14	4.58	1.11
platelet glycoprotein Ib alpha chain precursor [Homo sapiens]	0.99	4.14	4.29	1.04
voltage-dependent calcium channel subunit alpha-2/delta-2 isoform c precursor [Homo sapiens]	2.49	11.30	11.75	1.04
L-lactate dehydrogenase B chain [Homo sapiens]	0.89	0.60	0.60	1.00
monocyte differentiation antigen CD14 precursor [Homo sapiens]	1.74	5.69	6.33	1.11
dmX-like protein 2 isoform 1 [Homo sapiens]	0.93	9.72	12.08	1.24
dmX-like protein 2 isoform 3 [Homo sapiens]	0.93	9.72	12.08	1.24
dystroglycan preproprotein [Homo sapiens]	0.92	3.82	4.23	1.11
hyaluronan-binding protein 2 isoform 2 [Homo sapiens]	0.97	4.17	4.26	1.02

adiponectin precursor [Homo sapiens]	2.24	4.33	7.07	1.63
serum amyloid A-1 protein preproprotein [Homo sapiens]	1.64	1.46	2.30	1.58
acyl-CoA-binding protein isoform 5 [Homo sapiens]	1.38	0.35	0.29	0.81
acyl-CoA-binding protein isoform 6 [Homo sapiens]	1.38	0.35	0.29	0.81
angiotensin-converting enzyme isoform 3 precursor [Homo sapiens]	1.28	5.38	4.78	0.89
acyl-CoA-binding protein isoform 4 [Homo sapiens]	1.38	0.35	0.29	0.81
complement C2 isoform 3 [Homo sapiens]	1.74	7.33	6.14	0.84
immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]	0.97	0.21	1.51	7.07
multiple inositol polyphosphate phosphatase 1 isoform 2 precursor [Homo sapiens]	1.37	19.79	20.69	1.05
multiple inositol polyphosphate phosphatase 1 isoform 3 [Homo sapiens]	1.22	9.89	11.03	1.11
glycogenin-1 isoform 2 [Homo sapiens]	1.26	0.17	0.37	2.18
glucose-6-phosphate isomerase isoform 1 [Homo sapiens]	2.17	0.19	0.16	0.81
fibrinogen beta chain isoform 2 preproprotein [Homo sapiens]	1.71	0.13	0.11	0.85
V-set and immunoglobulin domain-containing protein 4 isoform 4 precursor [Homo sapiens]	0.77	0.59	0.76	1.13
V-set and immunoglobulin domain-containing protein 4 isoform 3 precursor [Homo sapiens]	0.67	0.41	0.67	1.30
rho GDP-dissociation inhibitor 1 isoform b [Homo sapiens]	2.79	0.14	0.15	1.13
cytochrome b5 isoform 3 [Homo sapiens]	0.79	0.45	0.34	0.79
matrix Gla protein isoform 1 precursor [Homo sapiens]	1.74	3.38	4.84	1.43
interleukin-6 receptor subunit beta isoform 3 precursor [Homo sapiens]	0.68	0.74	0.63	0.84
cysteine-rich secretory protein 3 isoform 1 precursor [Homo sapiens]	1.19	2.32	2.44	1.05
cysteine-rich secretory protein 3 isoform 2 precursor [Homo sapiens]	1.19	2.32	2.44	1.05
glutathione S-transferase omega-1	1.38	0.39	0.49	1.27

isoform 2 [Homo sapiens]				
glutathione S-transferase omega-1				
isoform 3 [Homo sapiens]	1.37	0.44	0.44	1.00
coronin-1A [Homo sapiens]	1.74	0.14	0.11	0.78
serine/threonine-protein				
phosphatase 2A activator isoform e				
[Homo sapiens]	0.89	0.26	0.16	0.64
tubulin alpha-8 chain isoform 2				
[Homo sapiens]	0.77	0.14	0.15	0.96
zinc transporter 6 isoform 1 [Homo				
sapiens]	0.71	1.93	1.82	0.98
zinc transporter 6 isoform 3 [Homo				
sapiens]	0.71	1.93	1.82	0.98
zinc transporter 6 isoform 4 [Homo				
sapiens]	0.71	1.93	1.82	0.98
annexin A6 isoform 2 [Homo				
sapiens]	1.71	0.20	0.14	0.74
L-xylulose reductase isoform 2				
[Homo sapiens]	0.73	1.43	1.54	0.99
glutathione reductase, mitochondrial				
isoform 2 precursor [Homo sapiens]	2.60	1.11	1.00	0.90
glutathione reductase, mitochondrial				
isoform 3 precursor [Homo sapiens]	2.60	1.11	1.00	0.90
glutathione reductase, mitochondrial				
isoform 4 precursor [Homo sapiens]	2.60	1.11	1.00	0.90
spectrin alpha chain, non-				
erythrocytic 1 isoform 3 [Homo				
sapiens]	1.28	0.60	0.46	0.77
trypsin-3 isoform 4 preproprotein				
[Homo sapiens]	0.76	0.63	0.62	0.93
glutamate--cysteine ligase catalytic				
subunit isoform b [Homo sapiens]	0.65	0.50	0.52	0.98
tubulin beta-3 chain isoform 2				
[Homo sapiens]	1.27	0.26	0.28	1.10
extracellular matrix protein 2				
isoform 2 precursor [Homo sapiens]	0.93	4.76	2.82	0.59
extracellular matrix protein 2				
isoform 3 precursor [Homo sapiens]	0.93	4.76	2.82	0.59
lamin-B1 isoform 2 [Homo sapiens]	0.96	0.08	0.06	0.68
nucleoside diphosphate kinase B				
isoform b [Homo sapiens]	0.91	0.18	0.13	0.72
actin-related protein 2/3 complex				
subunit 4 isoform c [Homo sapiens]	0.88	0.13	0.11	0.85
ARPC4-TTLL3 fusion protein [Homo				
sapiens]	0.88	0.13	0.11	0.85
malate dehydrogenase, cytoplasmic				
isoform 1 [Homo sapiens]	0.88	0.68	0.46	0.68
malate dehydrogenase, cytoplasmic	0.88	0.68	0.46	0.68

isoform 3 [Homo sapiens]				
lactotransferrin isoform 2 [Homo sapiens]	1.57	0.10	0.08	0.83
stathmin-2 isoform 1 [Homo sapiens]	0.83	0.18	0.13	0.74
cathepsin S isoform 2 preproprotein [Homo sapiens]	1.55	0.59	0.61	1.02
SAA2-SAA2 protein precursor [Homo sapiens]	0.76	0.73	0.76	0.97
serum amyloid A-4 protein precursor [Homo sapiens]	0.76	0.73	0.76	0.97
proteasome subunit alpha type-5 isoform 2 [Homo sapiens]	1.28	3.66	6.69	1.83
vascular cell adhesion protein 1 isoform c precursor [Homo sapiens]	2.24	4.76	5.63	1.18
actin, gamma-enteric smooth muscle isoform 2 precursor [Homo sapiens]	0.82	0.69	1.34	1.93
actin, cytoplasmic 2 [Homo sapiens]	0.88	0.17	0.17	1.03
asialoglycoprotein receptor 2 isoform d [Homo sapiens]	0.83	4.65	4.50	0.97
c-myc promoter-binding protein-1 isoform MBP-1 [Homo sapiens]	1.28	0.08	0.07	0.91
complement factor H-related protein 4 isoform 1 precursor [Homo sapiens]	0.88	1.32	1.62	1.23
complement factor H-related protein 4 isoform 2 precursor [Homo sapiens]	0.88	1.32	1.62	1.23
scaffold attachment factor B1 isoform 1 [Homo sapiens]	1.41	0.78	0.49	0.63
scaffold attachment factor B1 isoform 2 [Homo sapiens]	1.41	0.78	0.49	0.63
scaffold attachment factor B1 isoform 4 [Homo sapiens]	1.41	0.78	0.49	0.63
CD44 antigen isoform 6 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 7 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
CD44 antigen isoform 8 precursor [Homo sapiens]	1.28	5.46	4.31	0.79
extracellular matrix protein 1 isoform 3 precursor [Homo sapiens]	0.88	4.34	3.08	0.71
regulator of telomere elongation helicase 1 isoform 2 [Homo sapiens]	0.70	0.60	0.88	1.22
tumor protein p73 isoform j [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform e [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform h [Homo sapiens]	0.56	0.30	0.11	0.50

sapiens]				
tumor protein p73 isoform k [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform i [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform l [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform f [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform g [Homo sapiens]	0.56	0.30	0.11	0.50
tumor protein p73 isoform m [Homo sapiens]	0.56	0.30	0.11	0.50
amyloid beta A4 protein isoform i precursor [Homo sapiens]	0.99	6.19	3.99	0.65
amyloid beta A4 protein isoform h precursor [Homo sapiens]	0.99	6.19	3.99	0.65
amyloid beta A4 protein isoform j precursor [Homo sapiens]	0.99	3.59	3.36	0.94
vitamin D-binding protein isoform 1 precursor [Homo sapiens]	1.74	8.55	8.34	0.98
vitamin D-binding protein isoform 3 precursor [Homo sapiens]	1.74	8.55	8.34	0.98
vascular endothelial growth factor A isoform r [Homo sapiens]	1.19	0.26	0.19	0.73
cartilage acidic protein 1 isoform B precursor [Homo sapiens]	0.88	2.32	2.65	1.14
F-actin-capping protein subunit beta isoform 2 [Homo sapiens]	0.96	0.41	0.34	0.82
F-actin-capping protein subunit beta isoform 3 [Homo sapiens]	0.91	0.37	0.29	0.76
NSFL1 cofactor p47 isoform d [Homo sapiens]	0.78	0.44	0.34	0.80
pyruvate kinase PKM isoform c [Homo sapiens]	1.00	0.19	0.18	0.94
pyruvate kinase PKM isoform d [Homo sapiens]	0.99	0.20	0.18	0.94
pyruvate kinase PKM isoform e [Homo sapiens]	0.99	0.19	0.20	1.01
pyruvate kinase PKM isoform f [Homo sapiens]	1.00	0.19	0.18	0.94
trans-Golgi network integral membrane protein 2 isoform 2 precursor [Homo sapiens]	1.43	11.66	11.58	0.99
trans-Golgi network integral membrane protein 2 isoform 3 precursor [Homo sapiens]	1.43	11.66	11.58	0.99
trans-Golgi network integral	1.43	11.66	11.58	0.99

membrane protein 2 isoform 4 precursor [Homo sapiens]				
receptor-type tyrosine-protein phosphatase beta isoform c precursor [Homo sapiens]	0.88	1.12	1.18	1.06
receptor-type tyrosine-protein phosphatase beta isoform d precursor [Homo sapiens]	0.88	1.12	1.18	1.06
atractin isoform 4 [Homo sapiens]	0.84	2.47	5.16	2.09
kallikrein-7 isoform 2 [Homo sapiens]	1.58	0.41	0.99	2.40
cadherin-13 isoform 2 [Homo sapiens]	1.28	1.50	1.47	0.98
cadherin-13 isoform 3 precursor [Homo sapiens]	0.95	1.49	1.47	0.98
cadherin-13 isoform 5 precursor [Homo sapiens]	2.60	1.50	1.34	0.89
cadherin-13 isoform 6 precursor [Homo sapiens]	2.60	1.50	1.34	0.89
glial fibrillary acidic protein isoform 3 [Homo sapiens]	2.07	0.13	0.07	0.56
neural cell adhesion molecule 1 isoform 5 precursor [Homo sapiens]	0.99	3.27	3.52	1.08
neural cell adhesion molecule 1 isoform 4 precursor [Homo sapiens]	0.99	3.27	3.52	1.08
HLA class I histocompatibility antigen, A-1 alpha chain precursor [Homo sapiens]	0.81	2.02	2.41	1.63
complement C4-B-like preproprotein [Homo sapiens]	0.88	4.43	3.43	0.77
phospholipid transfer protein isoform c precursor [Homo sapiens]	1.27	1.68	1.43	0.85
phospholipid transfer protein isoform d [Homo sapiens]	1.27	1.33	1.31	0.99
DEP domain-containing protein 5 isoform 5 [Homo sapiens]	1.43	0.77	1.44	1.88
lymphocyte-specific protein 1 isoform 3 [Homo sapiens]	0.95	0.23	0.24	1.04
HLA class I histocompatibility antigen, Cw-1 alpha chain precursor [Homo sapiens]	0.99	0.65	1.18	1.83
apolipoprotein B receptor [Homo sapiens]	0.81	0.05	0.75	6.15
kallikrein-7 isoform 3 [Homo sapiens]	1.58	0.41	0.99	2.40
fructose-bisphosphate aldolase A isoform 2 [Homo sapiens]	0.88	0.26	0.22	0.82
interleukin-18 isoform 2 proprotein [Homo sapiens]	0.97	0.10	0.08	0.77
trypsin-3 isoform 3 preproprotein	0.76	0.63	0.62	0.93

[Homo sapiens]				
CD166 antigen isoform 2 precursor				
[Homo sapiens]	1.74	3.51	2.73	0.78
CD166 antigen isoform 3 precursor				
[Homo sapiens]	1.74	3.51	2.73	0.78
nectin-3 isoform 2 precursor [Homo sapiens]	1.28	6.44	6.36	0.99
nectin-3 isoform 3 [Homo sapiens]	1.28	6.44	6.36	0.99
amyloid-like protein 2 isoform 5				
[Homo sapiens]	2.49	9.52	5.88	0.62
cofilin-2 isoform 2 [Homo sapiens]	1.19	0.08	0.07	0.91
scavenger receptor cysteine-rich type 1 protein M130 isoform a precursor [Homo sapiens]	0.95	1.41	1.26	0.90
scavenger receptor cysteine-rich type 1 protein M130 isoform b precursor [Homo sapiens]	0.95	1.41	1.26	0.90
arginase-1 isoform 1 [Homo sapiens]	1.74	0.47	0.40	0.87
low affinity immunoglobulin gamma Fc region receptor III-B isoform 1 [Homo sapiens]	2.11	1.39	3.11	2.24
cathelicidin antimicrobial peptide preproprotein [Homo sapiens]	1.26	0.18	0.12	0.68
thioredoxin isoform 2 [Homo sapiens]	2.60	0.21	0.16	0.76
neuropilin-1 isoform d precursor [Homo sapiens]	0.95	3.93	3.77	0.96
neuropilin-1 isoform e precursor [Homo sapiens]	0.95	3.93	3.77	0.96
osteopontin isoform 4 precursor [Homo sapiens]	2.60	2.15	2.00	0.93
osteopontin isoform 5 [Homo sapiens]	2.60	2.15	2.00	0.93
ras-related protein Rap-1b isoform 2 [Homo sapiens]	0.95	0.11	0.08	0.72
ras-related protein Rap-1b isoform 3 [Homo sapiens]	0.95	0.11	0.08	0.72
ras-related protein Rap-1b isoform 4 [Homo sapiens]	0.95	0.11	0.08	0.72
clusterin preproprotein [Homo sapiens]	0.84	3.71	4.07	1.10
complement C4-A isoform 2 preproprotein [Homo sapiens]	2.60	9.32	4.63	0.50
neural cell adhesion molecule L1-like protein isoform 2 precursor [Homo sapiens]	2.60	2.08	3.90	1.87
contactin-1 isoform 3 precursor [Homo sapiens]	1.90	3.13	3.22	1.03

myosin-10 isoform 2 [Homo sapiens]	1.27	0.73	0.41	0.56
myosin-10 isoform 3 [Homo sapiens]	1.27	0.73	0.41	0.56
vitamin K-dependent protein Z				
isoform 1 precursor [Homo sapiens]	1.28	1.95	1.62	0.83
macrophage-capping protein isoform 2 [Homo sapiens]	1.34	0.13	0.11	0.85
apolipoprotein M isoform 2 [Homo sapiens]	0.70	2.49	1.23	0.59
protein flightless-1 homolog isoform 2 [Homo sapiens]	2.30	0.27	0.22	0.80
protein flightless-1 homolog isoform 3 [Homo sapiens]	2.30	0.27	0.22	0.80
keratin, type II cytoskeletal 8 isoform 1 [Homo sapiens]	0.79	0.14	0.15	1.25
keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]	0.79	0.14	0.15	1.25
immunoglobulin lambda-like polypeptide 5 isoform 2 [Homo sapiens]	0.97	0.21	1.48	7.04
ubiquitin-conjugating enzyme E2 L3 isoform 3 [Homo sapiens]	1.28	0.18	0.14	0.83
ubiquitin-conjugating enzyme E2 L3 isoform 4 [Homo sapiens]	1.28	0.18	0.14	0.83
leukotriene A-4 hydrolase isoform 3 [Homo sapiens]	0.83	0.20	0.16	0.80
leukotriene A-4 hydrolase isoform 2 [Homo sapiens]	0.83	0.20	0.16	0.80
glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]	1.79	0.15	0.12	0.85
vesicle-trafficking protein SEC22b precursor [Homo sapiens]	0.76	0.09	0.08	0.87
amyloid beta A4 precursor protein-binding family B member 1 isoform g [Homo sapiens]	2.49	43.95	58.97	1.34
amyloid beta A4 precursor protein-binding family B member 1 isoform f [Homo sapiens]	2.49	43.95	58.97	1.34
amyloid beta A4 precursor protein-binding family B member 1 isoform e [Homo sapiens]	2.49	43.95	58.97	1.34
amyloid beta A4 precursor protein-binding family B member 1 isoform d [Homo sapiens]	2.49	43.95	58.97	1.34
ubiquitin-conjugating enzyme E2 variant 1 isoform e [Homo sapiens]	0.84	0.10	0.13	1.33
ubiquitin-conjugating enzyme E2 variant 1 isoform f [Homo sapiens]	0.84	0.10	0.13	1.33

V-set and immunoglobulin domain-containing protein 4 isoform 5 precursor [Homo sapiens]	0.77	0.59	0.76	1.13
triosephosphate isomerase isoform 3 [Homo sapiens]	2.79	0.16	0.12	0.74
transketolase isoform 2 [Homo sapiens]	1.43	0.30	0.20	0.65
gelsolin isoform d [Homo sapiens]	0.99	6.68	6.72	1.00
selenium-binding protein 1 isoform 2 [Homo sapiens]	0.65	0.37	0.35	0.97
selenium-binding protein 1 isoform 3 [Homo sapiens]	0.63	0.35	0.21	0.68
radixin isoform 1 [Homo sapiens]	1.21	0.20	0.14	0.74
radixin isoform 3 [Homo sapiens]	1.21	0.20	0.14	0.74
interleukin-1 receptor type 2 isoform 2 precursor [Homo sapiens]	2.49	2.50	1.62	0.65
exostosin-like 2 isoform 3 [Homo sapiens]	0.83	8.27	8.34	1.01
chitotriosidase-1 isoform 2 precursor [Homo sapiens]	3.57	1.58	1.76	1.11
coagulation factor VII isoform c preproprotein [Homo sapiens]	0.88	4.76	4.39	0.92
gelsolin isoform f [Homo sapiens]	0.99	6.68	6.72	1.00
UV excision repair protein RAD23 homolog A isoform 2 [Homo sapiens]	0.64	0.18	0.14	0.80
UV excision repair protein RAD23 homolog A isoform 3 [Homo sapiens]	0.64	0.18	0.14	0.80
inactive tyrosine-protein kinase 7 isoform e [Homo sapiens]	0.88	1.42	1.41	0.99
tubulin alpha-1A chain isoform 1 [Homo sapiens]	0.81	0.08	0.08	1.18
tubulin alpha-1A chain isoform 2 [Homo sapiens]	0.81	0.08	0.08	1.18
actin-related protein 2/3 complex subunit 5 isoform 2 [Homo sapiens]	0.84	0.26	0.23	0.88
proteasome subunit beta type-6 isoform 2 proprotein [Homo sapiens]	2.60	2.14	0.93	0.43
chitotriosidase-1 isoform 3 precursor [Homo sapiens]	3.57	1.58	1.76	1.11
low affinity immunoglobulin gamma Fc region receptor III-B isoform 3 [Homo sapiens]	2.11	1.39	3.11	2.24
low affinity immunoglobulin gamma Fc region receptor III-B isoform 4 [Homo sapiens]	2.11	1.39	3.11	2.24
low affinity immunoglobulin gamma Fc region receptor III-B isoform 5 [Homo sapiens]	2.73	0.58	1.28	2.19

brain acid soluble protein 1 [Homo sapiens]	1.80	0.17	0.15	0.88
PREDICTED: low affinity immunoglobulin gamma Fc region receptor III-A-like isoform X1 [Homo sapiens]	2.19	3.58	5.49	1.53
PREDICTED: prothymosin alpha-like [Homo sapiens]	1.92	0.85	0.41	0.48
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	2.07	0.18	0.12	0.69
putative macrophage stimulating 1-like protein [Homo sapiens]	1.43	6.08	5.53	0.91
cytoplasmic dynein 1 intermediate chain 2 isoform 2 [Homo sapiens]	0.65	0.05	0.50	4.42
cytoplasmic dynein 1 intermediate chain 2 isoform 1 [Homo sapiens]	0.65	0.05	0.50	4.42
cytoplasmic dynein 1 intermediate chain 2 isoform 3 [Homo sapiens]	0.65	0.05	0.50	4.42
trem-like transcript 1 protein isoform b precursor [Homo sapiens]	0.92	4.26	5.57	1.31
gelsolin isoform e [Homo sapiens]	0.99	6.68	6.72	1.00
multiple epidermal growth factor-like domains protein 8 isoform 1 precursor [Homo sapiens]	1.43	5.46	5.76	1.05
heat shock protein HSP 90-beta isoform b [Homo sapiens]	0.74	0.18	0.19	0.99
heat shock protein HSP 90-beta isoform c [Homo sapiens]	0.74	0.18	0.19	0.99
syntaxin-binding protein 2 isoform c [Homo sapiens]	1.26	0.06	0.05	0.83
myc-associated zinc finger protein isoform 3 [Homo sapiens]	0.83	1.90	1.98	1.04
POTE ankyrin domain family member J [Homo sapiens]	0.91	0.18	0.18	0.99
actin-related protein 3 isoform 2 [Homo sapiens]	0.83	0.26	0.27	1.02
WD repeat-containing protein 72 isoform a [Homo sapiens]	0.40	1.61	0.75	0.57
transgelin-2 isoform b [Homo sapiens]	0.95	1.33	1.25	0.94
transgelin-2 isoform a [Homo sapiens]	0.95	1.33	1.25	0.94
POTE ankyrin domain family member I [Homo sapiens]	0.91	0.18	0.18	0.99
membrane primary amine oxidase isoform 2 [Homo sapiens]	1.27	5.34	4.33	0.81
membrane primary amine oxidase isoform 3 [Homo sapiens]	1.69	0.36	0.34	0.93

spectrin beta chain, non-erythrocytic 5 [Homo sapiens]	0.83	0.74	0.34	0.46
endoglin isoform 3 [Homo sapiens]	1.28	2.08	2.05	0.99
tropomyosin alpha-3 chain isoform 6 [Homo sapiens]	1.26	0.20	0.20	1.02
tropomyosin alpha-3 chain isoform 7 [Homo sapiens]	1.35	0.21	0.20	0.97
tropomyosin alpha-3 chain isoform 8 [Homo sapiens]	1.35	0.21	0.20	0.97
tropomyosin alpha-3 chain isoform 9 [Homo sapiens]	1.24	0.20	0.20	1.02
neutral alpha-glucosidase AB isoform 4 [Homo sapiens]	2.49	0.73	0.51	0.71
neutral alpha-glucosidase AB isoform 5 [Homo sapiens]	2.49	0.73	0.51	0.71
neutral alpha-glucosidase AB isoform 6 [Homo sapiens]	2.49	0.73	0.51	0.71
alpha-actinin-2 isoform 2 [Homo sapiens]	0.81	0.21	0.24	1.34
alpha-actinin-2 isoform 3 [Homo sapiens]	0.81	0.21	0.24	1.34
annexin A11 isoform 2 [Homo sapiens]	1.54	0.36	0.39	1.08
carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	1.58	4.36	4.16	0.96
carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	1.58	4.38	4.19	0.96
actin-related protein 2/3 complex subunit 3 isoform 1 [Homo sapiens]	1.58	0.29	0.27	0.96
complement component C8 beta chain isoform 1 preproprotein [Homo sapiens]	1.74	5.59	6.39	1.14
complement component C8 beta chain isoform 2 [Homo sapiens]	1.74	5.59	6.39	1.14
complement component C8 beta chain isoform 3 [Homo sapiens]	1.74	5.59	6.39	1.14
hsc70-interacting protein isoform 2 [Homo sapiens]	0.84	0.47	0.37	0.79
ran-specific GTPase-activating protein isoform 1 [Homo sapiens]	1.00	0.56	0.14	0.26
ran-specific GTPase-activating protein isoform 3 [Homo sapiens]	1.00	0.56	0.14	0.26
ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	1.00	0.56	0.14	0.26
neutrophil cytosol factor 1 [Homo sapiens]	0.82	0.11	0.14	1.24
polyubiquitin-B precursor [Homo sapiens]	1.74	0.34	0.39	1.15

biotinidase isoform 1 [Homo sapiens]	0.97	6.65	7.74	1.16
biotinidase isoform 2 [Homo sapiens]	0.97	6.65	7.74	1.16
biotinidase isoform 5 [Homo sapiens]	0.96	7.14	7.96	1.11
peptidylprolyl isomerase A (cyclophilin A)-like 4E [Homo sapiens]	1.74	0.17	0.12	0.74
PREDICTED: LOW QUALITY PROTEIN: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	2.07	0.18	0.12	0.69
PREDICTED: tubulin alpha-3E chain-like [Homo sapiens]	0.71	0.08	0.08	1.18
PREDICTED: myosin regulatory light chain 12B-like [Homo sapiens]	0.88	0.25	0.39	1.58
PREDICTED: GDH/6PGL endoplasmic bifunctional protein isoform X2 [Homo sapiens]	1.40	3.28	3.32	1.01
PREDICTED: GDH/6PGL endoplasmic bifunctional protein isoform X3 [Homo sapiens]	1.40	3.28	3.32	1.01
PREDICTED: alkaline phosphatase, tissue-nonspecific isozyme isoform X3 [Homo sapiens]	0.76	2.14	1.39	0.78
PREDICTED: tissue alpha-L-fucosidase isoform X1 [Homo sapiens]	1.54	1.50	0.71	0.48
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X3 [Homo sapiens]	2.32	0.85	0.41	0.48
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X5 [Homo sapiens]	2.32	0.85	0.41	0.48
PREDICTED: heterochromatin protein 1-binding protein 3 isoform X8 [Homo sapiens]	2.32	0.85	0.41	0.48
PREDICTED: PITH domain-containing protein 1 isoform X1 [Homo sapiens]	0.79	0.04	0.65	6.58
PREDICTED: EF-hand domain-containing protein D2 isoform X1 [Homo sapiens]	0.97	0.11	0.10	0.90
PREDICTED: exostosin-like 2 isoform X2 [Homo sapiens]	0.83	8.27	8.34	1.01
PREDICTED: alpha-amylase 1 isoform X2 [Homo sapiens]	2.07	1.79	1.94	1.09
PREDICTED: nuclease-sensitive element-binding protein 1 isoform X1 [Homo sapiens]	2.24	0.05	0.98	19.85
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X2	0.96	1.09	1.47	1.36

[Homo sapiens]				
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X3				
[Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X4				
[Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X5				
[Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: synaptonemal complex protein 1 isoform X2 [Homo sapiens]	1.28	3.61	3.63	1.01
PREDICTED: synaptonemal complex protein 1 isoform X3 [Homo sapiens]	1.28	3.61	3.63	1.01
PREDICTED: synaptonemal complex protein 1 isoform X4 [Homo sapiens]	1.28	3.61	3.63	1.01
PREDICTED: T-cell acute lymphocytic leukemia protein 1 isoform X2				
[Homo sapiens]	1.00	5.58	8.85	1.59
PREDICTED: complement component C8 beta chain isoform X1 [Homo sapiens]	1.74	5.59	6.39	1.14
PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	0.76	1.49	1.36	0.89
PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sapiens]	0.77	1.49	1.36	0.89
PREDICTED: low affinity immunoglobulin gamma Fc region receptor II-a isoform X1 [Homo sapiens]	0.81	1.41	1.51	0.99
PREDICTED: complement factor H-related protein 2 isoform X1 [Homo sapiens]	0.89	3.56	7.06	1.98
PREDICTED: laminin subunit gamma-2 isoform X1 [Homo sapiens]	2.21	0.13	0.07	0.55
PREDICTED: antithrombin-III isoform X1 [Homo sapiens]	2.24	6.44	5.81	0.90
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X1 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X2 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X3 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X4	1.52	3.03	3.12	1.03

[Homo sapiens]				
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X6 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X7 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X8 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: pyruvate kinase PKLR isoform X1 [Homo sapiens]	1.28	0.21	0.19	0.90
PREDICTED: nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 isoform X1 [Homo sapiens]	6.20	0.31	0.16	0.52
PREDICTED: CD5 antigen-like isoform X1 [Homo sapiens]	1.55	0.90	0.75	0.84
PREDICTED: BRO1 domain-containing protein BROX isoform X1 [Homo sapiens]	0.81	0.08	0.81	4.45
PREDICTED: BRO1 domain-containing protein BROX isoform X5 [Homo sapiens]	0.81	0.08	0.81	4.45
PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo sapiens]	0.91	2.52	2.28	0.90
PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sapiens]	0.99	5.34	6.15	1.15
PREDICTED: C4b-binding protein beta chain isoform X2 [Homo sapiens]	1.43	8.81	9.18	1.04
PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]	0.97	4.16	4.99	1.20
PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]	0.99	3.14	4.65	1.48
PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X1 [Homo sapiens]	1.43	3.23	2.27	0.70
PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X2 [Homo sapiens]	1.43	3.23	2.27	0.70
PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X3 [Homo sapiens]	1.28	1.78	1.59	0.89

PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X4 [Homo sapiens]	1.28	1.78	1.59	0.89
PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]	1.90	3.32	2.44	0.73
PREDICTED: V-type proton ATPase subunit B, kidney isoform isoform X1 [Homo sapiens]	0.60	0.26	0.29	1.58
PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	2.24	3.52	2.53	0.72
PREDICTED: UTP--glucose-1-phosphate uridylyltransferase isoform X2 [Homo sapiens]	0.99	0.78	0.52	0.67
PREDICTED: macrophage-capping protein isoform X1 [Homo sapiens]	1.34	0.13	0.11	0.85
PREDICTED: tyrosine-protein kinase Mer isoform X1 [Homo sapiens]	1.28	7.33	9.20	1.26
PREDICTED: tyrosine-protein kinase Mer isoform X4 [Homo sapiens]	1.28	7.33	9.20	1.26
PREDICTED: vitamin K-dependent protein C isoform X1 [Homo sapiens]	1.50	18.99	12.51	0.66
PREDICTED: vitamin K-dependent protein C isoform X2 [Homo sapiens]	1.50	18.99	12.51	0.66
PREDICTED: vitamin K-dependent protein C isoform X3 [Homo sapiens]	1.50	18.99	12.51	0.66
PREDICTED: collagen alpha-3(IV) chain isoform X1 [Homo sapiens]	1.52	8.57	17.16	2.00
PREDICTED: collagen alpha-3(IV) chain isoform X2 [Homo sapiens]	1.52	8.57	17.16	2.00
PREDICTED: collagen alpha-3(IV) chain isoform X3 [Homo sapiens]	1.52	8.57	17.16	2.00
PREDICTED: collagen alpha-3(IV) chain isoform X5 [Homo sapiens]	1.52	8.57	17.16	2.00
PREDICTED: collagen alpha-3(IV) chain isoform X6 [Homo sapiens]	1.52	8.57	17.16	2.00
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X2 [Homo sapiens]	0.65	0.05	0.50	4.42
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X3 [Homo sapiens]	0.65	0.05	0.50	4.42
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X4 [Homo sapiens]	0.65	0.05	0.50	4.42
PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X7	0.65	0.05	0.50	4.42

[Homo sapiens]				
PREDICTED: dipeptidyl peptidase 4 isoform X1 [Homo sapiens]	1.58	3.47	3.47	1.00
PREDICTED: fibronectin isoform X1 [Homo sapiens]	2.60	5.94	2.32	0.39
PREDICTED: fibronectin isoform X2 [Homo sapiens]	2.60	5.95	2.31	0.39
PREDICTED: fibronectin isoform X3 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X4 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X5 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X6 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X7 [Homo sapiens]	2.60	5.94	2.32	0.39
PREDICTED: fibronectin isoform X8 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X9 [Homo sapiens]	2.60	5.94	2.32	0.39
PREDICTED: fibronectin isoform X10 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X11 [Homo sapiens]	2.60	6.07	2.31	0.38
PREDICTED: fibronectin isoform X12 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X13 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X14 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X15 [Homo sapiens]	2.60	6.07	2.31	0.38
PREDICTED: fibronectin isoform X16 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X17 [Homo sapiens]	2.60	6.07	2.31	0.38
PREDICTED: fibronectin isoform X18 [Homo sapiens]	2.60	5.95	2.31	0.39
PREDICTED: fibronectin isoform X19 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X20 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: fibronectin isoform X21 [Homo sapiens]	2.60	5.94	2.31	0.39
PREDICTED: grancalcin isoform X1 [Homo sapiens]	0.91	0.07	0.05	0.73
PREDICTED: glia-derived nexin	0.79	2.30	2.61	1.29

isoform X1 [Homo sapiens]				
PREDICTED: glia-derived nexin				
isoform X2 [Homo sapiens]	0.79	2.30	2.61	1.29
PREDICTED: dedicator of cytokinesis				
protein 10 isoform X1 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: dedicator of cytokinesis				
protein 10 isoform X2 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: tubulin alpha-4A chain				
isoform X1 [Homo sapiens]	0.77	0.14	0.15	0.96
PREDICTED: collagen alpha-3(VI)				
chain isoform X1 [Homo sapiens]	0.79	2.59	1.51	0.66
PREDICTED: collagen alpha-3(VI)				
chain isoform X2 [Homo sapiens]	0.79	2.59	1.51	0.66
PREDICTED: secreted				
phosphoprotein 24 isoform X1				
[Homo sapiens]	0.89	3.27	3.75	1.15
PREDICTED: sushi, nidogen and EGF-				
like domain-containing protein 1				
isoform X1 [Homo sapiens]	0.83	1.64	2.39	1.46
PREDICTED: filamin-B isoform X1				
[Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: filamin-B isoform X2				
[Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: filamin-B isoform X5				
[Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: filamin-B isoform X6				
[Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: acylamino-acid-releasing				
enzyme isoform X1 [Homo sapiens]	0.74	0.26	0.20	0.81
PREDICTED: acylamino-acid-releasing				
enzyme isoform X2 [Homo sapiens]	0.74	0.26	0.20	0.81
PREDICTED: inter-alpha-trypsin				
inhibitor heavy chain H3 isoform X1				
[Homo sapiens]	2.49	6.40	8.87	1.39
PREDICTED: receptor-type tyrosine-				
protein phosphatase gamma isoform				
X1 [Homo sapiens]	0.99	5.98	6.82	1.14
PREDICTED: receptor-type tyrosine-				
protein phosphatase gamma isoform				
X2 [Homo sapiens]	0.99	5.98	6.82	1.14
PREDICTED: tetranectin isoform X1				
[Homo sapiens]	0.95	6.95	4.26	0.61
PREDICTED: voltage-dependent				
calcium channel subunit alpha-				
2/delta-2 isoform X1 [Homo sapiens]	2.49	11.30	11.75	1.04
PREDICTED: target of Nesh-SH3	0.82	2.55	1.58	0.62

isoform X1 [Homo sapiens]				
PREDICTED: target of Nesh-SH3				
isoform X2 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X3 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X4 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X5 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X6 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X7 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X8 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X9 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X10 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X11 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X13 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X14 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X15 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X16 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X17 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X18 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X19 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X20 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X21 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X22 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X23 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X25 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X26 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3	0.82	2.55	1.58	0.62

isoform X27 [Homo sapiens]				
PREDICTED: target of Nesh-SH3				
isoform X28 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X29 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X30 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X31 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X32 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X33 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X34 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X35 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X36 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X37 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3				
isoform X38 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: poliovirus receptor-related protein 3 isoform X1 [Homo sapiens]	1.28	6.44	6.36	0.99
PREDICTED: poliovirus receptor-related protein 3 isoform X2 [Homo sapiens]	1.28	6.44	6.36	0.99
PREDICTED: fetuin-B isoform X3 [Homo sapiens]	1.28	5.64	5.03	0.89
PREDICTED: fetuin-B isoform X4 [Homo sapiens]	1.28	5.43	5.03	0.93
PREDICTED: Golgi integral membrane protein 4 isoform X1 [Homo sapiens]	0.88	2.28	1.98	0.87
PREDICTED: Golgi integral membrane protein 4 isoform X2 [Homo sapiens]	0.88	2.28	1.98	0.87
PREDICTED: Golgi integral membrane protein 4 isoform X3 [Homo sapiens]	0.88	2.28	1.98	0.87
PREDICTED: histidine-rich glycoprotein isoform X1 [Homo sapiens]	1.43	7.33	6.20	0.85
PREDICTED: interleukin-1 receptor accessory protein isoform X2 [Homo sapiens]	1.58	3.23	6.50	2.02
PREDICTED: limbic system-associated membrane protein isoform X1 [Homo sapiens]	2.07	3.04	2.37	0.78

PREDICTED: ELL-associated factor 2 isoform X1 [Homo sapiens]	2.44	0.18	0.13	0.71
PREDICTED: vitamin K-dependent protein S isoform X1 [Homo sapiens]	1.90	5.42	5.90	1.09
PREDICTED: protein HEG homolog 1 isoform X1 [Homo sapiens]	0.88	9.52	9.86	1.04
PREDICTED: cholinesterase isoform X1 [Homo sapiens]	0.99	4.52	5.54	1.23
PREDICTED: tumor protein 63 isoform X1 [Homo sapiens]	0.56	0.30	0.11	0.50
PREDICTED: tumor protein 63 isoform X2 [Homo sapiens]	0.56	0.30	0.11	0.50
PREDICTED: tumor protein 63 isoform X4 [Homo sapiens]	0.56	0.30	0.11	0.50
PREDICTED: ADP-ribosyl cyclase 2 isoform X1 [Homo sapiens]	1.72	3.32	2.58	0.78
PREDICTED: ADP-ribosyl cyclase 2 isoform X2 [Homo sapiens]	1.72	3.32	2.58	0.78
PREDICTED: ADP-ribosyl cyclase 2 isoform X3 [Homo sapiens]	1.72	3.32	2.58	0.78
PREDICTED: mast/stem cell growth factor receptor Kit isoform X1 [Homo sapiens]	1.41	2.82	2.00	0.71
PREDICTED: mast/stem cell growth factor receptor Kit isoform X2 [Homo sapiens]	1.41	2.82	2.00	0.71
PREDICTED: mast/stem cell growth factor receptor Kit isoform X3 [Homo sapiens]	1.41	2.82	2.00	0.71
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X1 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X2 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X3 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X4 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X5 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-processing factor FIP1 isoform X6 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end-	3.12	0.26	0.22	0.86

processing factor FIP1 isoform X7 [Homo sapiens]				
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X8 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X9 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X10 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X13 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X14 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: pre-mRNA 3'-end- processing factor FIP1 isoform X15 [Homo sapiens]	3.12	0.26	0.22	0.86
PREDICTED: platelet factor 4 isoform X1 [Homo sapiens]	1.90	2.98	3.18	1.07
PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	0.99	4.11	4.80	1.17
PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	0.99	4.15	4.66	1.12
PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	0.96	4.20	4.82	1.15
PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	0.99	3.88	4.27	1.10
PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	1.00	4.11	4.54	1.10
PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	0.99	3.82	3.57	0.94
PREDICTED: histone H2A.Z isoform X1 [Homo sapiens]	4.00	0.13	0.09	0.66
PREDICTED: complement factor I isoform X1 [Homo sapiens]	5.87	77.98	68.08	0.87
PREDICTED: plasma kallikrein isoform X1 [Homo sapiens]	1.58	5.96	5.58	0.94
PREDICTED: endomucin isoform X1 [Homo sapiens]	1.31	10.71	15.71	1.47
PREDICTED: myosin regulatory light chain 12B-like [Homo sapiens]	0.88	0.25	0.39	1.58
PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]	0.76	0.28	0.28	0.94
PREDICTED: complement component C6 isoform X1 [Homo sapiens]	1.43	6.21	6.15	0.99

PREDICTED: complement component C6 isoform X2 [Homo sapiens]	1.43	6.22	6.21	1.00
PREDICTED: oncostatin-M-specific receptor subunit beta isoform X1 [Homo sapiens]	0.81	0.69	0.80	1.48
PREDICTED: oncostatin-M-specific receptor subunit beta isoform X3 [Homo sapiens]	0.81	0.69	0.80	1.48
PREDICTED: oncostatin-M-specific receptor subunit beta isoform X4 [Homo sapiens]	0.81	0.69	0.80	1.48
PREDICTED: interleukin-6 receptor subunit beta isoform X1 [Homo sapiens]	0.68	0.74	0.63	0.84
PREDICTED: annexin A6 isoform X2 [Homo sapiens]	1.74	0.21	0.14	0.67
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X2 [Homo sapiens]	0.83	0.05	0.05	0.90
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X6 [Homo sapiens]	0.83	0.05	0.05	0.90
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X7 [Homo sapiens]	0.83	0.05	0.05	0.90
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X10 [Homo sapiens]	0.83	0.05	0.05	0.90
PREDICTED: platelet-derived growth factor receptor beta isoform X1 [Homo sapiens]	0.54	0.53	0.61	1.36
PREDICTED: nucleophosmin isoform X2 [Homo sapiens]	1.58	0.42	0.32	0.76
PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Homo sapiens]	1.35	13.00	9.94	0.76
PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Homo sapiens]	1.35	13.00	9.94	0.76
PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Homo sapiens]	1.35	13.00	9.94	0.76
PREDICTED: peptidase inhibitor 16 isoform X3 [Homo sapiens]	1.43	3.78	4.18	1.11

PREDICTED: protein YIPF3 isoform X1 [Homo sapiens]	0.93	2.39	2.44	1.02
PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]	0.70	1.54	1.45	0.95
PREDICTED: histone H2B type 1-D isoform X1 [Homo sapiens]	3.33	0.13	0.07	0.51
PREDICTED: major histocompatibility complex, class I, B isoform X1 [Homo sapiens]	0.81	1.42	1.65	1.43
PREDICTED: heat shock 70 kDa protein 1-like isoform X1 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: heat shock protein HSP 90-beta isoform X1 [Homo sapiens]	0.74	0.18	0.19	0.99
PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone] isoform X4 [Homo sapiens]	0.76	0.48	0.40	0.84
PREDICTED: serpin B9 isoform X1 [Homo sapiens]	2.66	0.37	0.35	0.95
PREDICTED: cysteine-rich secretory protein 2 isoform X1 [Homo sapiens]	1.40	12.27	17.13	1.40
PREDICTED: platelet-activating factor acetylhydrolase isoform X2 [Homo sapiens]	1.46	0.89	2.55	2.88
PREDICTED: CD109 antigen isoform X1 [Homo sapiens]	0.92	0.25	0.21	0.87
PREDICTED: laminin subunit alpha-2 isoform X1 [Homo sapiens]	0.70	4.20	3.24	0.79
PREDICTED: laminin subunit alpha-2 isoform X2 [Homo sapiens]	0.70	4.20	3.24	0.79
PREDICTED: mannosyl-oligosaccharide 1,2-alpha-mannosidase IA isoform X1 [Homo sapiens]	0.96	4.04	4.06	1.00
PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X1 [Homo sapiens]	0.76	0.07	0.65	4.25
PREDICTED: peptidyl-prolyl cis-trans isomerase A isoform X1 [Homo sapiens]	2.60	0.25	0.20	0.80
PREDICTED: extracellular serine/threonine protein kinase FAM20C isoform X1 [Homo sapiens]	1.19	2.55	2.54	1.00

PREDICTED: WD repeat-containing protein 91 isoform X1 [Homo sapiens]	0.88	2.94	4.65	1.58
PREDICTED: serrate RNA effector molecule homolog isoform X2 [Homo sapiens]	1.74	2.91	2.80	0.96
PREDICTED: serrate RNA effector molecule homolog isoform X3 [Homo sapiens]	1.74	2.91	2.80	0.96
PREDICTED: serrate RNA effector molecule homolog isoform X4 [Homo sapiens]	1.74	2.91	2.80	0.96
PREDICTED: serrate RNA effector molecule homolog isoform X5 [Homo sapiens]	1.74	2.91	2.80	0.96
PREDICTED: neurosecretory protein VGF isoform X2 [Homo sapiens]	0.82	3.08	3.15	0.96
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X2 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X4 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X5 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X6 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: retinoic acid receptor responder protein 2 isoform X2 [Homo sapiens]	1.58	6.17	5.98	0.97
PREDICTED: acid ceramidase isoform X1 [Homo sapiens]	2.46	0.48	0.46	0.96
PREDICTED: testis-expressed sequence 15 protein isoform X3 [Homo sapiens]	1.94	3.76	3.84	1.02
PREDICTED: stathmin-4 isoform X1 [Homo sapiens]	0.84	0.15	0.09	0.60
PREDICTED: stathmin-4 isoform X4 [Homo sapiens]	0.84	0.15	0.09	0.60
PREDICTED: stathmin-2 isoform X2 [Homo sapiens]	0.83	0.18	0.13	0.74
PREDICTED: protein FAM49B isoform X4 [Homo sapiens]	0.89	0.46	0.50	1.10
PREDICTED: plectin isoform X1 [Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X2	1.37	0.35	0.27	0.76

[Homo sapiens]				
PREDICTED: plectin isoform X3				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X4				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X5				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X6				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X7				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X8				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X9				
[Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: GDP-L-fucose synthase isoform X1 [Homo sapiens]	1.34	0.25	0.21	0.87
PREDICTED: GDP-L-fucose synthase isoform X2 [Homo sapiens]	1.34	0.25	0.21	0.87
PREDICTED: GDP-L-fucose synthase isoform X3 [Homo sapiens]	1.34	0.25	0.21	0.87
PREDICTED: 14-3-3 protein zeta/delta isoform X1 [Homo sapiens]	0.81	0.18	0.14	0.88
PREDICTED: 14-3-3 protein zeta/delta isoform X3 [Homo sapiens]	0.81	0.18	0.14	0.88
PREDICTED: beta-1,4-galactosyltransferase 1 isoform X1 [Homo sapiens]	0.88	4.33	4.15	0.96
PREDICTED: trypsin-3 isoform X1 [Homo sapiens]	0.76	0.63	0.62	0.93
PREDICTED: talin-1 isoform X1 [Homo sapiens]	1.38	0.27	0.39	1.41
PREDICTED: tropomyosin beta chain isoform X3 [Homo sapiens]	2.79	0.77	0.63	0.82
PREDICTED: tropomyosin beta chain isoform X5 [Homo sapiens]	2.79	0.77	0.63	0.82
PREDICTED: tropomyosin beta chain isoform X6 [Homo sapiens]	2.79	0.77	0.63	0.82
PREDICTED: tropomyosin beta chain isoform X7 [Homo sapiens]	2.79	0.77	0.63	0.82
PREDICTED: adenylate kinase isoenzyme 1 isoform X1 [Homo sapiens]	4.25	0.29	0.27	0.91
PREDICTED: adenylate kinase isoenzyme 1 isoform X3 [Homo sapiens]	4.25	0.29	0.27	0.91

PREDICTED: delta-aminolevulinic acid dehydratase isoform X1 [Homo sapiens]	0.56	0.13	0.10	0.80
PREDICTED: Golgin subfamily A member 2 isoform X1 [Homo sapiens]	4.25	1.51	1.20	0.80
PREDICTED: Golgin subfamily A member 2 isoform X2 [Homo sapiens]	4.25	1.51	1.20	0.80
PREDICTED: Golgin subfamily A member 2 isoform X3 [Homo sapiens]	4.25	1.51	1.20	0.80
PREDICTED: gelsolin isoform X1 [Homo sapiens]	0.99	6.68	6.72	1.00
PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X5 [Homo sapiens]	0.95	0.30	0.27	0.90
PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]	0.95	0.30	0.27	0.90
PREDICTED: tenascin isoform X1 [Homo sapiens]	0.83	1.23	1.56	1.26
PREDICTED: tenascin isoform X2 [Homo sapiens]	0.84	1.13	1.45	1.29
PREDICTED: tenascin isoform X3 [Homo sapiens]	0.82	1.25	1.68	1.35
PREDICTED: tenascin isoform X4 [Homo sapiens]	0.84	1.26	1.45	1.15
PREDICTED: actin-related protein 2/3 complex subunit 5-like protein isoform X1 [Homo sapiens]	0.78	0.44	0.40	0.89
PREDICTED: annexin A11 isoform X1 [Homo sapiens]	1.54	0.36	0.39	1.08
PREDICTED: annexin A11 isoform X2 [Homo sapiens]	1.54	0.36	0.39	1.08
PREDICTED: cartilage acidic protein 1 isoform X1 [Homo sapiens]	0.88	2.32	2.65	1.14
PREDICTED: retinol-binding protein 4 isoform X1 [Homo sapiens]	1.18	9.18	10.84	1.18
PREDICTED: vinculin isoform X1 [Homo sapiens]	1.21	0.49	0.48	0.99
PREDICTED: vinculin isoform X2 [Homo sapiens]	1.21	0.49	0.48	0.99
PREDICTED: hemopexin isoform X1 [Homo sapiens]	1.19	9.77	9.46	0.97
PREDICTED: lymphocyte-specific protein 1 isoform X1 [Homo sapiens]	0.95	0.23	0.24	1.04
PREDICTED: lymphocyte-specific	0.95	0.23	0.24	1.04

protein 1 isoform X4 [Homo sapiens]				
PREDICTED: CD44 antigen isoform X1 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X2 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X3 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X4 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X5 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X8 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X9 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X10 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: interleukin-18-binding protein isoform X2 [Homo sapiens]	1.18	5.96	5.51	0.92
PREDICTED: peroxiredoxin-5, mitochondrial isoform X1 [Homo sapiens]	0.97	0.53	0.32	0.61
PREDICTED: hypoxia up-regulated protein 1 isoform X5 [Homo sapiens]	1.27	3.76	3.84	1.02
PREDICTED: cell adhesion molecule 1 isoform X1 [Homo sapiens]	0.99	0.20	0.19	0.96
PREDICTED: cell adhesion molecule 1 isoform X2 [Homo sapiens]	0.99	0.20	0.19	0.96
PREDICTED: cell adhesion molecule 1 isoform X3 [Homo sapiens]	0.99	0.20	0.19	0.96
PREDICTED: cell adhesion molecule 1 isoform X4 [Homo sapiens]	0.99	0.20	0.19	0.96
PREDICTED: cell surface glycoprotein MUC18 isoform X1 [Homo sapiens]	1.90	3.26	3.37	1.03
PREDICTED: cell surface glycoprotein MUC18 isoform X2 [Homo sapiens]	1.00	4.41	4.48	1.02
PREDICTED: complement C1s subcomponent isoform X1 [Homo sapiens]	2.49	9.48	6.92	0.73
PREDICTED: complement C1r subcomponent-like protein isoform X2 [Homo sapiens]	1.19	9.59	10.57	1.10
PREDICTED: complement C1r subcomponent-like protein isoform X3 [Homo sapiens]	1.19	9.59	10.57	1.10
PREDICTED: scavenger receptor cysteine-rich type 1 protein M130 isoform X2 [Homo sapiens]	0.95	1.67	1.42	0.85

PREDICTED: scavenger receptor cysteine-rich type 1 protein M130 isoform X3 [Homo sapiens]	0.95	1.41	1.26	0.90
PREDICTED: dermcidin isoform X1 [Homo sapiens]	0.88	0.18	0.23	1.27
PREDICTED: heterogeneous nuclear ribonucleoprotein A1 isoform X1 [Homo sapiens]	0.73	0.07	0.04	0.75
PREDICTED: insulin-like growth factor I isoform X1 [Homo sapiens]	1.28	7.34	8.34	1.14
PREDICTED: keratin, type II cytoskeletal 3 isoform X1 [Homo sapiens]	0.68	0.11	0.11	0.94
PREDICTED: leukotriene A-4 hydrolase isoform X1 [Homo sapiens]	0.83	0.20	0.16	0.80
PREDICTED: bridging integrator 2 isoform X1 [Homo sapiens]	1.24	4.69	3.70	0.79
PREDICTED: bridging integrator 2 isoform X2 [Homo sapiens]	1.24	4.69	3.70	0.79
PREDICTED: peripherin isoform X1 [Homo sapiens]	0.62	0.09	0.08	0.85
PREDICTED: periostin isoform X2 [Homo sapiens]	2.79	0.85	1.21	1.42
PREDICTED: periostin isoform X3 [Homo sapiens]	2.79	0.85	1.21	1.42
PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	1.58	4.38	4.19	0.96
PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	1.58	4.36	4.16	0.96
PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	1.19	22.88	23.40	1.02
PREDICTED: S-formylglutathione hydrolase isoform X1 [Homo sapiens]	1.58	1.36	1.40	1.03
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X1 [Homo sapiens]	1.58	0.11	0.10	0.92
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X2 [Homo sapiens]	1.58	0.11	0.10	0.92
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X3 [Homo sapiens]	1.58	0.11	0.10	0.92
PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X4 [Homo sapiens]	1.58	0.11	0.10	0.92
PREDICTED: high mobility group protein B1 isoform X3 [Homo sapiens]	1.27	0.30	0.28	0.92

PREDICTED: high mobility group protein B1 isoform X6 [Homo sapiens]	1.27	0.30	0.28	0.92
PREDICTED: glia maturation factor beta isoform X1 [Homo sapiens]	0.99	0.14	0.11	0.83
PREDICTED: proteasome subunit beta type-5 isoform X1 [Homo sapiens]	0.71	0.28	0.32	1.44
PREDICTED: dmX-like protein 2 isoform X1 [Homo sapiens]	0.93	9.72	12.08	1.24
PREDICTED: dmX-like protein 2 isoform X2 [Homo sapiens]	0.93	9.72	12.08	1.24
PREDICTED: dmX-like protein 2 isoform X3 [Homo sapiens]	0.93	9.72	12.08	1.24
PREDICTED: dmX-like protein 2 isoform X4 [Homo sapiens]	0.93	9.72	12.08	1.24
PREDICTED: SHC-transforming protein 4 isoform X1 [Homo sapiens]	1.43	20.57	13.57	0.66
PREDICTED: neogenin isoform X1 [Homo sapiens]	1.35	4.14	4.58	1.11
PREDICTED: neogenin isoform X3 [Homo sapiens]	1.35	4.14	4.58	1.11
PREDICTED: neogenin isoform X4 [Homo sapiens]	1.35	4.14	4.58	1.11
PREDICTED: neogenin isoform X6 [Homo sapiens]	1.35	4.14	4.58	1.11
PREDICTED: neogenin isoform X8 [Homo sapiens]	1.35	4.14	4.58	1.11
PREDICTED: dual oxidase 2 isoform X1 [Homo sapiens]	0.73	0.30	0.29	0.92
PREDICTED: spectrin beta chain, non-erythrocytic 5 isoform X1 [Homo sapiens]	0.83	0.74	0.34	0.46
PREDICTED: pyruvate kinase PKM isoform X1 [Homo sapiens]	0.99	0.20	0.18	0.92
PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	0.99	0.20	0.18	0.92
PREDICTED: dual oxidase 1 isoform X1 [Homo sapiens]	0.81	0.30	0.24	0.82
PREDICTED: beta-2-microglobulin isoform X1 [Homo sapiens]	0.99	4.43	6.41	1.45
PREDICTED: tropomyosin alpha-1 chain isoform X11 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1 chain isoform X12 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1 chain isoform X13 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1	1.94	0.73	0.63	0.85

chain isoform X14 [Homo sapiens]				
PREDICTED: tropomyosin alpha-1				
chain isoform X15 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1				
chain isoform X16 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1				
chain isoform X17 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: tropomyosin alpha-1				
chain isoform X18 [Homo sapiens]	1.94	0.73	0.63	0.85
PREDICTED: talin-2 isoform X8				
[Homo sapiens]	1.90	0.68	0.88	1.30
PREDICTED: semaphorin-4B isoform				
X1 [Homo sapiens]	2.60	2.53	2.33	0.92
PREDICTED: aminopeptidase N				
isoform X1 [Homo sapiens]	1.26	2.27	2.45	1.08
PREDICTED: hemoglobin subunit zeta				
isoform X1 [Homo sapiens]	0.60	0.50	0.29	0.65
PREDICTED: eukaryotic translation				
initiation factor 5A-1 isoform X5				
[Homo sapiens]	0.99	0.26	0.23	0.88
PREDICTED: protein flightless-1				
homolog isoform X1 [Homo sapiens]	2.30	0.27	0.22	0.80
PREDICTED: protein flightless-1				
homolog isoform X2 [Homo sapiens]	2.30	0.27	0.22	0.80
PREDICTED: protein flightless-1				
homolog isoform X4 [Homo sapiens]	2.30	0.27	0.22	0.80
PREDICTED: asialoglycoprotein				
receptor 2 isoform X1 [Homo				
sapiens]	0.83	4.65	4.50	0.97
PREDICTED: myosin-10 isoform X1				
[Homo sapiens]	1.27	0.73	0.41	0.56
PREDICTED: myosin-10 isoform X2				
[Homo sapiens]	1.27	0.73	0.41	0.56
PREDICTED: myosin-10 isoform X3				
[Homo sapiens]	1.27	0.73	0.41	0.56
PREDICTED: alpha-2-antiplasmin				
isoform X1 [Homo sapiens]	2.24	6.75	6.22	0.92
PREDICTED: alpha-2-antiplasmin				
isoform X2 [Homo sapiens]	2.24	6.75	6.22	0.92
PREDICTED: alpha-2-antiplasmin				
isoform X3 [Homo sapiens]	2.24	6.75	6.22	0.92
PREDICTED: alpha-2-antiplasmin				
isoform X6 [Homo sapiens]	2.24	6.75	6.22	0.92
PREDICTED: sex hormone-binding				
globulin isoform X3 [Homo sapiens]	0.96	3.37	3.44	1.02
PREDICTED: sex hormone-binding				
globulin isoform X6 [Homo sapiens]	0.99	4.00	5.66	1.42
PREDICTED: fructose-bisphosphate	0.88	0.18	0.13	0.71

aldolase C isoform X1 [Homo sapiens]				
PREDICTED: fructose-bisphosphate aldolase C isoform X3 [Homo sapiens]	0.88	0.18	0.13	0.71
PREDICTED: putative sodium-coupled neutral amino acid transporter 10 isoform X1 [Homo sapiens]	1.44	8.27	9.04	1.09
PREDICTED: angiotensin-converting enzyme isoform X1 [Homo sapiens]	1.28	5.38	4.78	0.89
PREDICTED: keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]	0.40	0.29	0.41	1.28
PREDICTED: keratin, type I cytoskeletal 17 isoform X1 [Homo sapiens]	0.60	0.10	0.07	0.75
PREDICTED: ATP-citrate synthase isoform X1 [Homo sapiens]	0.99	0.78	0.63	0.81
PREDICTED: ATP-citrate synthase isoform X2 [Homo sapiens]	0.99	0.78	0.63	0.81
PREDICTED: ATP-citrate synthase isoform X3 [Homo sapiens]	0.99	0.78	0.63	0.81
PREDICTED: cadherin-2 isoform X1 [Homo sapiens]	0.97	2.10	1.86	0.89
PREDICTED: cadherin-2 isoform X2 [Homo sapiens]	0.97	2.10	1.86	0.89
PREDICTED: desmocollin-2 isoform X1 [Homo sapiens]	1.00	1.71	1.83	1.07
PREDICTED: tropomyosin alpha-4 chain isoform X1 [Homo sapiens]	1.28	0.77	0.63	0.82
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X1 [Homo sapiens]	1.74	0.34	0.39	1.15
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X2 [Homo sapiens]	1.74	0.34	0.39	1.15
PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X4 [Homo sapiens]	1.74	0.34	0.39	1.15
PREDICTED: creatine kinase M-type isoform X1 [Homo sapiens]	0.68	0.69	0.90	1.13
PREDICTED: zinc finger protein 548 isoform X1 [Homo sapiens]	1.82	0.08	0.07	0.82
PREDICTED: glyceraldehyde-3-phosphate dehydrogenase, testis-specific isoform X1 [Homo sapiens]	1.55	0.18	0.13	0.74
PREDICTED: glucose-6-phosphate	2.17	0.19	0.16	0.81

isomerase isoform X2 [Homo sapiens]				
PREDICTED: apolipoprotein E isoform X1 [Homo sapiens]	0.99	5.82	3.61	0.62
PREDICTED: poliovirus receptor isoform X1 [Homo sapiens]	1.18	7.34	8.79	1.20
PREDICTED: vasodilator-stimulated phosphoprotein isoform X1 [Homo sapiens]	1.61	0.08	0.04	0.51
PREDICTED: vasodilator-stimulated phosphoprotein isoform X2 [Homo sapiens]	1.31	0.18	0.18	1.01
PREDICTED: alpha-actinin-4 isoform X1 [Homo sapiens]	0.88	0.28	0.21	0.76
PREDICTED: alpha-actinin-4 isoform X2 [Homo sapiens]	0.88	0.28	0.21	0.76
PREDICTED: calpain small subunit 1 isoform X1 [Homo sapiens]	2.07	0.26	0.24	0.91
PREDICTED: calpain small subunit 1 isoform X3 [Homo sapiens]	2.07	0.26	0.24	0.91
PREDICTED: glia maturation factor gamma isoform X1 [Homo sapiens]	0.99	0.14	0.11	0.83
PREDICTED: glutathione synthetase isoform X2 [Homo sapiens]	1.74	0.73	0.61	0.83
PREDICTED: phospholipid transfer protein isoform X1 [Homo sapiens]	1.27	1.68	1.43	0.85
PREDICTED: bactericidal permeability-increasing protein isoform X1 [Homo sapiens]	2.70	0.22	0.18	0.83
PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isoform X1 [Homo sapiens]	1.54	0.56	0.21	0.38
PREDICTED: ICOS ligand isoform X1 [Homo sapiens]	0.84	3.62	5.08	1.40
PREDICTED: heparin cofactor 2 isoform X1 [Homo sapiens]	1.43	7.33	5.97	0.82
PREDICTED: neurofilament heavy polypeptide isoform X1 [Homo sapiens]	1.00	0.35	0.44	1.26
PREDICTED: apolipoprotein L1 isoform X1 [Homo sapiens]	0.62	0.68	0.56	0.84
PREDICTED: DEP domain-containing protein 5 isoform X1 [Homo sapiens]	1.43	0.77	1.44	1.88
PREDICTED: DEP domain-containing protein 5 isoform X3 [Homo sapiens]	1.43	0.77	1.44	1.88
PREDICTED: DEP domain-containing protein 5 isoform X4 [Homo sapiens]	1.43	0.77	1.44	1.88
PREDICTED: peroxiredoxin-4 isoform	0.89	0.35	0.35	1.01

X1 [Homo sapiens]				
PREDICTED: moesin isoform X1 [Homo sapiens]	1.19	0.13	0.11	0.85
PREDICTED: coagulation factor IX isoform X2 [Homo sapiens]	1.28	8.82	7.85	0.89
PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X1 [Homo sapiens]	0.97	0.11	0.15	1.41
PREDICTED: glucose-6-phosphate 1-dehydrogenase isoform X2 [Homo sapiens]	0.97	0.11	0.15	1.41
PREDICTED: liver carboxylesterase 1 isoform X1 [Homo sapiens]	1.69	6.12	1.35	0.22
PREDICTED: haptoglobin isoform X1 [Homo sapiens]	0.88	0.70	0.16	0.23
PREDICTED: myosin regulatory light chain 12A isoform X2 [Homo sapiens]	0.82	0.15	0.19	1.29
PREDICTED: neutrophil elastase isoform X1 [Homo sapiens]	1.79	0.17	0.15	0.88
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X1 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X8 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X11 [Homo sapiens]	0.65	3.27	2.71	0.83
PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]	0.76	0.34	0.40	1.54
PREDICTED: attractin isoform X1 [Homo sapiens]	0.84	2.47	5.16	2.09
PREDICTED: attractin isoform X2 [Homo sapiens]	0.83	3.57	3.42	0.96
PREDICTED: coagulation factor X isoform X1 [Homo sapiens]	1.58	3.99	3.08	0.77
PREDICTED: argininosuccinate synthase isoform X1 [Homo sapiens]	0.79	1.26	0.77	0.68
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X1 [Homo sapiens]	0.92	0.85	0.46	0.54
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X2 [Homo sapiens]	0.92	0.85	0.46	0.54
PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X3	0.92	0.85	0.46	0.54

[Homo sapiens]				
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo sapiens]	0.89	0.26	0.27	1.02
PREDICTED: HLA class I histocompatibility antigen, B-44 alpha chain isoform X1 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, B-15 alpha chain isoform X1 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, B-18 alpha chain isoform X1 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, B-18 alpha chain isoform X2 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X4 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	2.79	0.08	0.06	0.73
PREDICTED: HLA class I histocompatibility antigen, B-44 alpha chain isoform X1 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X2 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: liver carboxylesterase 1 isoform X1 [Homo sapiens]	1.69	6.12	1.35	0.22
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	2.07	0.18	0.12	0.69
PREDICTED: myosin regulatory light chain 12B-like [Homo sapiens]	0.88	0.25	0.39	1.58

PREDICTED: prothymosin alpha-like [Homo sapiens]	0.62	0.04	0.07	1.32
F-actin-capping protein subunit beta isoform 4 [Homo sapiens]	0.96	0.25	0.27	1.08
adenosine deaminase CECR1 isoform a precursor [Homo sapiens]	0.88	1.81	2.19	1.21
adenosine deaminase CECR1 isoform c [Homo sapiens]	0.88	1.81	2.19	1.21
adenosine deaminase CECR1 isoform d [Homo sapiens]	0.88	1.81	2.19	1.21
proteasome subunit alpha type-6 isoform c [Homo sapiens]	0.88	0.16	0.20	1.22
plastin-3 isoform 3 [Homo sapiens]	1.19	0.28	0.19	0.68
plastin-3 isoform 4 [Homo sapiens]	1.19	0.28	0.19	0.68
isocitrate dehydrogenase [NADP] cytoplasmic [Homo sapiens]	1.90	2.07	0.50	0.24
complement C2 isoform 4 [Homo sapiens]	1.90	4.61	5.79	1.26
complement C2 isoform 5 [Homo sapiens]	1.74	4.28	7.84	1.83
complement C2 isoform 6 precursor [Homo sapiens]	0.99	3.02	3.58	1.18
synaptonemal complex protein 1 isoform 2 [Homo sapiens]	1.28	3.61	3.63	1.01
ubiquitin-conjugating enzyme E2 variant 1 isoform i [Homo sapiens]	0.84	0.10	0.13	1.33
GDH/6PGL endoplasmic bifunctional protein isoform 1 precursor [Homo sapiens]	1.40	3.28	3.32	1.01
noelin isoform 5 [Homo sapiens]	1.27	2.18	2.46	1.13
noelin isoform 4 precursor [Homo sapiens]	1.27	2.18	2.46	1.13
stress-induced-phosphoprotein 1 isoform a [Homo sapiens]	0.91	0.90	1.65	1.83
stress-induced-phosphoprotein 1 isoform c [Homo sapiens]	0.84	0.75	0.88	1.16
lamin isoform C [Homo sapiens]	0.76	0.30	0.20	0.71
lamin isoform A-delta50 [Homo sapiens]	0.76	0.30	0.20	0.71
acyl-CoA-binding protein isoform 1 [Homo sapiens]	1.38	0.35	0.29	0.81
plexin domain-containing protein 2 isoform 2 [Homo sapiens]	0.93	3.81	3.87	1.02
COP9 signalosome complex subunit 7b isoform a [Homo sapiens]	0.67	7.11	6.15	0.86
COP9 signalosome complex subunit 7b isoform d [Homo sapiens]	0.67	7.11	6.15	0.86
COP9 signalosome complex subunit	0.67	7.11	6.15	0.86

7b isoform c [Homo sapiens]				
COP9 signalosome complex subunit				
7b isoform e [Homo sapiens]	0.67	7.11	6.15	0.86
stathmin-4 isoform 3 [Homo sapiens]	0.84	0.15	0.09	0.60
stathmin-4 isoform 4 [Homo sapiens]	0.84	0.15	0.09	0.60
stathmin-4 isoform 2 [Homo sapiens]	0.84	0.15	0.09	0.60
ICOS ligand isoform b precursor [Homo sapiens]	0.84	3.62	5.08	1.40
regulator of telomere elongation helicase 1 isoform 3 [Homo sapiens]	0.70	0.60	0.88	1.22
regulator of telomere elongation helicase 1 isoform 4 [Homo sapiens]	0.70	0.60	0.88	1.22
calpastatin isoform n [Homo sapiens]	0.58	0.26	0.24	0.88
calpastatin isoform o [Homo sapiens]	0.58	0.26	0.24	0.88
drebrin-like protein isoform d [Homo sapiens]	0.88	0.42	0.41	0.98
drebrin-like protein isoform e [Homo sapiens]	0.88	0.42	0.41	0.98
calponin-3 isoform 2 [Homo sapiens]	0.71	0.17	0.15	0.87
cholesteryl ester transfer protein isoform 2 precursor [Homo sapiens]	1.27	7.24	3.32	0.46
periostin isoform 6 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
periostin isoform 5 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
periostin isoform 7 precursor [Homo sapiens]	2.79	0.85	1.21	1.42
alcohol dehydrogenase 1B isoform 2 [Homo sapiens]	0.93	2.03	0.69	0.34
kelch-like protein 1 isoform 2 [Homo sapiens]	0.32	0.26		
actin-related protein 2/3 complex subunit 3 isoform 2 [Homo sapiens]	1.58	0.29	0.27	0.96
chloride intracellular channel protein 1 [Homo sapiens]	0.70	0.15	0.13	0.87
BRO1 domain-containing protein BROX isoform c [Homo sapiens]	0.81	0.08	0.81	4.45
ADAMTS-like protein 4 isoform 3 precursor [Homo sapiens]	1.58	8.41	6.97	0.83
ADAMTS-like protein 4 isoform 4 precursor [Homo sapiens]	1.58	8.41	6.97	0.83
cystatin-C precursor [Homo sapiens]	0.74	3.71	4.14	1.16
macrophage colony-stimulating factor 1 receptor precursor [Homo sapiens]	0.89	4.45	3.07	0.69
kallistatin isoform 1 [Homo sapiens]	1.00	4.63	4.88	1.05
kallistatin isoform 2 precursor [Homo	1.00	4.63	4.88	1.05

sapiens]				
glucosidase 2 subunit beta isoform 2 precursor [Homo sapiens]	1.52	0.80	0.76	0.95
glucosidase 2 subunit beta isoform 3 precursor [Homo sapiens]	1.52	0.80	0.76	0.95
sex hormone-binding globulin isoform 5 [Homo sapiens]	1.74	3.45	5.11	1.48
sex hormone-binding globulin isoform 6 [Homo sapiens]	1.74	4.43	4.07	0.92
sex hormone-binding globulin isoform 7 [Homo sapiens]	2.24	6.58	8.98	1.36
tubulin beta-4A chain isoform 1 [Homo sapiens]	0.77	0.18	0.14	0.78
tubulin beta-4A chain isoform 2 [Homo sapiens]	0.77	0.18	0.14	0.78
tubulin beta-4A chain isoform 4 [Homo sapiens]	0.60	0.05	0.04	0.76
glucose-6-phosphate isomerase isoform 3 [Homo sapiens]	2.17	0.19	0.16	0.81
glucose-6-phosphate isomerase isoform 4 [Homo sapiens]	2.17	0.19	0.16	0.81
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	0.78	0.75	1.92	1.76
PREDICTED: ICOS ligand-like isoform X1 [Homo sapiens]	0.84	3.62	5.08	1.40
PREDICTED: uncharacterized protein LOC100293211 [Homo sapiens]	0.97	0.29	0.76	2.65
PREDICTED: putative trypsin-6-like [Homo sapiens]	0.97	1.26	1.24	0.98
PREDICTED: low affinity immunoglobulin gamma Fc region receptor III-A-like isoform X2 [Homo sapiens]	2.19	3.58	5.49	1.53
PREDICTED: adenylyl cyclase-associated protein 1 isoform X3 [Homo sapiens]	2.60	0.14	0.14	1.02
PREDICTED: mannosyl-oligosaccharide 1,2-alpha-mannosidase IB isoform X1 [Homo sapiens]	1.58	14.72	13.92	0.95
PREDICTED: alpha-enolase isoform X1 [Homo sapiens]	1.28	0.09	0.15	1.57
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X6 [Homo sapiens]	0.95	2.98	3.19	1.07

PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X7 [Homo sapiens]	0.95	2.98	3.19	1.07
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X8 [Homo sapiens]	0.95	2.98	3.19	1.07
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X9 [Homo sapiens]	0.95	2.98	3.19	1.07
PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X10 [Homo sapiens]	0.96	2.38	2.73	1.15
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X7 [Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X8 [Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X9 [Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X10 [Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X11 [Homo sapiens]	0.96	1.09	1.47	1.36
PREDICTED: receptor-type tyrosine-protein phosphatase F isoform X12 [Homo sapiens]	0.45	1.09	1.47	1.16
PREDICTED: serine/arginine-rich splicing factor 4 isoform X1 [Homo sapiens]	0.82	0.39		
PREDICTED: complement component C8 beta chain isoform X2 [Homo sapiens]	1.74	5.59	6.39	1.14
PREDICTED: F-actin-capping protein subunit beta isoform X1 [Homo sapiens]	0.96	0.41	0.34	0.82
PREDICTED: GDH/6PGL endoplasmic bifunctional protein isoform X4 [Homo sapiens]	1.40	3.28	3.32	1.01
PREDICTED: proteoglycan 4 isoform X2 [Homo sapiens]	0.88	2.31	2.20	0.96

PREDICTED: proteoglycan 4 isoform X1 [Homo sapiens]	0.88	2.31	2.20	0.96
PREDICTED: complement factor H-related protein 4 isoform X1 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X2 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X3 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X4 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X5 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: complement factor H-related protein 4 isoform X7 [Homo sapiens]	0.88	1.32	1.62	1.23
PREDICTED: BRO1 domain-containing protein BROX isoform X6 [Homo sapiens]	0.81	0.08	0.81	4.45
PREDICTED: cyclic AMP-dependent transcription factor ATF-6 alpha isoform X1 [Homo sapiens]	1.43	4.67	3.87	0.83
PREDICTED: cyclic AMP-dependent transcription factor ATF-6 alpha isoform X2 [Homo sapiens]	1.43	4.67	3.87	0.83
PREDICTED: hepatoma-derived growth factor isoform X2 [Homo sapiens]	0.99	0.78	0.58	0.75
PREDICTED: complement factor H isoform X1 [Homo sapiens]	0.99	5.60	5.93	1.06
PREDICTED: complement factor H isoform X2 [Homo sapiens]	0.96	5.11	5.54	1.08
PREDICTED: complement factor H-related protein 1 isoform X1 [Homo sapiens]	2.60	4.64	3.20	0.69
PREDICTED: complement factor H-related protein 2 isoform X2 [Homo sapiens]	0.89	3.56	7.06	1.98
PREDICTED: protein S100-A7A isoform X1 [Homo sapiens]	1.43	0.06	0.75	13.25
PREDICTED: laminin subunit gamma-	2.21	0.13	0.07	0.55

2 isoform X2 [Homo sapiens]				
PREDICTED: histone H2B type 2-F isoform X1 [Homo sapiens]	3.33	0.13	0.07	0.51
PREDICTED: histone H2B type 2-F isoform X2 [Homo sapiens]	3.33	0.13	0.07	0.51
PREDICTED: protein phosphatase 1 regulatory subunit 12B isoform X9 [Homo sapiens]	1.52	3.03	3.12	1.03
PREDICTED: pyruvate kinase PKLR isoform X2 [Homo sapiens]	1.28	0.21	0.19	0.90
PREDICTED: ADAMTS-like protein 4 isoform X1 [Homo sapiens]	1.58	8.41	6.97	0.83
PREDICTED: ADAMTS-like protein 4 isoform X2 [Homo sapiens]	1.00	5.95	5.95	1.00
PREDICTED: tropomyosin alpha-3 chain isoform X1 [Homo sapiens]	1.26	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X2 [Homo sapiens]	1.26	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X3 [Homo sapiens]	1.26	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X5 [Homo sapiens]	1.24	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X6 [Homo sapiens]	1.26	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X7 [Homo sapiens]	1.24	0.20	0.20	1.02
PREDICTED: tropomyosin alpha-3 chain isoform X9 [Homo sapiens]	1.47	0.21	0.20	0.97
PREDICTED: nidogen-1 isoform X1 [Homo sapiens]	1.00	6.89	6.39	0.93
PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	2.07	0.18	0.12	0.69
PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X6 [Homo sapiens]	1.43	3.23	2.27	0.70
PREDICTED: zinc transporter 6 isoform X1 [Homo sapiens]	0.71	1.93	1.82	0.98
PREDICTED: zinc transporter 6 isoform X2 [Homo sapiens]	0.71	1.93	1.82	0.98
PREDICTED: zinc transporter 6 isoform X3 [Homo sapiens]	0.71	1.93	1.82	0.98
PREDICTED: UTP--glucose-1-phosphate uridylyltransferase isoform X4 [Homo sapiens]	0.99	0.63	0.51	0.82
PREDICTED: actin-related protein 2/3 complex subunit 2 isoform X1 [Homo sapiens]	0.91	0.48	0.38	0.80
PREDICTED: collagen alpha-3(IV)	1.52	8.57	17.16	2.00

chain isoform X8 [Homo sapiens] PREDICTED: collagen alpha-3(IV)				
chain isoform X9 [Homo sapiens] PREDICTED: collagen alpha-3(VI)	1.52	8.57	17.16	2.00
chain isoform X3 [Homo sapiens] PREDICTED: cytoplasmic dynein 1	0.79	2.59	1.51	0.66
intermediate chain 2 isoform X8 [Homo sapiens] PREDICTED: cytoplasmic dynein 1	0.65	0.05	0.50	4.42
intermediate chain 2 isoform X9 [Homo sapiens] PREDICTED: grancalcin isoform X2	0.65	0.05	0.50	4.42
[Homo sapiens] PREDICTED: grancalcin isoform X3	0.91	0.07	0.05	0.73
[Homo sapiens] PREDICTED: grancalcin isoform X4	0.91	0.07	0.05	0.73
[Homo sapiens] PREDICTED: grancalcin isoform X5	0.91	0.07	0.05	0.73
[Homo sapiens] PREDICTED: sushi, nidogen and EGF- like domain-containing protein 1	0.83	1.64	2.39	1.46
isoform X2 [Homo sapiens] PREDICTED: sushi, nidogen and EGF- like domain-containing protein 1	0.83	1.64	2.39	1.46
isoform X3 [Homo sapiens] PREDICTED: sushi, nidogen and EGF- like domain-containing protein 1	0.83	1.64	2.39	1.46
isoform X4 [Homo sapiens] PREDICTED: POTE ankyrin domain family member E isoform X1 [Homo sapiens]	0.88	0.16	0.15	0.94
PREDICTED: bifunctional purine biosynthesis protein PURH isoform X1 [Homo sapiens] PREDICTED: dedicator of cytokinesis protein 10 isoform X4 [Homo sapiens]	1.26	0.27	0.22	0.79
PREDICTED: dedicator of cytokinesis protein 10 isoform X5 [Homo sapiens] PREDICTED: dedicator of cytokinesis protein 10 isoform X6 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: dedicator of cytokinesis protein 10 isoform X7 [Homo sapiens] PREDICTED: dedicator of cytokinesis protein 10 isoform X8 [Homo	1.74	41.25	57.82	1.40
	1.74	41.25	57.82	1.40

sapiens]				
PREDICTED: dedicator of cytokinesis protein 10 isoform X9 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: dedicator of cytokinesis protein 10 isoform X10 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: dedicator of cytokinesis protein 10 isoform X11 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: dedicator of cytokinesis protein 10 isoform X12 [Homo sapiens]	1.74	41.25	57.82	1.40
PREDICTED: vitamin K-dependent protein C isoform X4 [Homo sapiens]	1.50	18.99	12.51	0.66
PREDICTED: COP9 signalosome complex subunit 7b isoform X1 [Homo sapiens]	0.67	7.11	6.15	0.86
PREDICTED: interleukin-1 receptor type 2 isoform X1 [Homo sapiens]	2.49	2.50	1.62	0.65
PREDICTED: interleukin-1 receptor type 2 isoform X2 [Homo sapiens]	2.49	2.50	1.62	0.65
PREDICTED: interleukin-1 receptor type 2 isoform X4 [Homo sapiens]	2.49	2.50	1.62	0.65
PREDICTED: uncharacterized protein LOC729468 [Homo sapiens]	1.35	0.47	2.73	5.76
PREDICTED: neural cell adhesion molecule L1-like protein isoform X2 [Homo sapiens]	2.60	2.08	3.90	1.87
PREDICTED: neural cell adhesion molecule L1-like protein isoform X4 [Homo sapiens]	2.60	2.08	3.90	1.87
PREDICTED: filamin-B isoform X7 [Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X2 [Homo sapiens]	2.49	6.40	8.87	1.39
PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X3 [Homo sapiens]	2.24	6.37	8.82	1.38
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Homo sapiens]	0.99	4.01	3.94	0.98
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Homo sapiens]	1.28	3.91	3.59	0.92
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Homo sapiens]	1.00	3.91	3.87	0.99

sapiens]				
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]	2.60	3.25	3.32	1.02
PREDICTED: biotinidase isoform X5 [Homo sapiens]	0.97	6.65	7.74	1.16
PREDICTED: transketolase isoform X1 [Homo sapiens]	1.43	0.26	0.20	0.77
PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X1 [Homo sapiens]	1.26	2.49	0.70	0.28
PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X2 [Homo sapiens]	1.26	2.49	0.70	0.28
PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X3 [Homo sapiens]	1.26	2.49	0.70	0.28
PREDICTED: cysteine-rich with EGF-like domain protein 1 isoform X4 [Homo sapiens]	1.26	2.49	0.70	0.28
PREDICTED: ceruloplasmin isoform X1 [Homo sapiens]	0.81	2.49	43.42	6.34
PREDICTED: ceruloplasmin isoform X2 [Homo sapiens]	0.81	2.49	43.42	6.34
PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]	0.81	2.49	43.42	6.34
PREDICTED: ceruloplasmin isoform X4 [Homo sapiens]	0.81	2.49	43.42	6.34
PREDICTED: target of Nesh-SH3 isoform X39 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X40 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X41 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X42 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X43 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X44 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X45 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X46 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: target of Nesh-SH3 isoform X47 [Homo sapiens]	0.82	2.55	1.58	0.62
PREDICTED: limbic system-associated membrane protein isoform X2	2.07	3.04	2.37	0.78

[Homo sapiens]				
PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Homo sapiens]	0.97	3.89	3.87	1.00
PREDICTED: WD repeat-containing protein 1 isoform X1 [Homo sapiens]	2.60	0.39	0.37	0.95
PREDICTED: mast/stem cell growth factor receptor Kit isoform X4 [Homo sapiens]	1.41	2.82	2.00	0.71
PREDICTED: afamin isoform X1 [Homo sapiens]	0.84	3.49	3.34	0.96
PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	0.99	4.11	4.80	1.17
PREDICTED: vitamin D-binding protein isoform X1 [Homo sapiens]	1.90	8.26	8.68	1.05
PREDICTED: complement factor I isoform X3 [Homo sapiens]	5.87	77.98	68.08	0.87
PREDICTED: complement factor I isoform X4 [Homo sapiens]	5.87	77.98	68.08	0.87
PREDICTED: immunoglobulin J chain isoform X2 [Homo sapiens]	2.83	0.73	1.31	1.78
PREDICTED: plasma kallikrein isoform X2 [Homo sapiens]	1.58	6.07	5.63	0.93
PREDICTED: complement component C6 isoform X3 [Homo sapiens]	1.43	6.21	6.15	0.99
PREDICTED: complement component C6 isoform X4 [Homo sapiens]	1.43	6.32	6.26	0.99
PREDICTED: cyclin-dependent kinase-like 3 isoform X6 [Homo sapiens]	0.83	3.93	3.84	0.98
PREDICTED: cyclin-dependent kinase-like 3 isoform X7 [Homo sapiens]	0.83	3.93	3.84	0.98
PREDICTED: cyclin-dependent kinase-like 3 isoform X9 [Homo sapiens]	0.83	3.93	3.84	0.98
PREDICTED: cyclin-dependent kinase-like 3 isoform X10 [Homo sapiens]	0.83	3.93	3.84	0.98
PREDICTED: calpastatin isoform X1 [Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X2 [Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X3 [Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X4 [Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X5	0.58	0.26	0.24	0.88

[Homo sapiens]				
PREDICTED: calpastatin isoform X6				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X7				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X8				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X9				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X10				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X11				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X12				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X13				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X14				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X15				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X16				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X17				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X18				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X19				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: calpastatin isoform X20				
[Homo sapiens]	0.58	0.26	0.24	0.88
PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X14				
[Homo sapiens]	0.83	0.05	0.05	0.90
PREDICTED: nucleophosmin isoform X3 [Homo sapiens]	1.58	0.42	0.32	0.76
PREDICTED: cadherin-related family member 2 isoform X1 [Homo sapiens]	0.96	1.31	0.96	0.73
PREDICTED: beta-synuclein isoform X1 [Homo sapiens]	0.46	0.04	0.04	0.93
PREDICTED: beta-synuclein isoform X3 [Homo sapiens]	0.46	0.04	0.04	0.93
PREDICTED: leukocyte elastase inhibitor isoform X1 [Homo sapiens]	2.37	0.24	0.22	0.91
PREDICTED: trem-like transcript 1 protein isoform X1 [Homo sapiens]	0.92	4.26	5.57	1.31

PREDICTED: ezrin isoform X1 [Homo sapiens]	0.83	0.39	0.25	0.63
PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]	0.76	0.07	0.65	4.25
PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	0.88	0.20	0.21	1.06
PREDICTED: actin-related protein 2/3 complex subunit 1B isoform X2 [Homo sapiens]	0.78	0.37	0.37	0.94
PREDICTED: filamin-C isoform X1 [Homo sapiens]	0.84	0.41	0.52	1.27
PREDICTED: hepatocyte growth factor receptor isoform X1 [Homo sapiens]	1.28	1.17	2.08	1.78
PREDICTED: hepatocyte growth factor receptor isoform X2 [Homo sapiens]	1.28	1.17	2.08	1.78
PREDICTED: hepatocyte growth factor receptor isoform X3 [Homo sapiens]	0.82	0.69	0.70	1.01
PREDICTED: serrate RNA effector molecule homolog isoform X6 [Homo sapiens]	1.74	2.91	2.80	0.96
PREDICTED: actin-related protein 3B isoform X1 [Homo sapiens]	0.82	0.22	0.19	0.86
PREDICTED: actin-related protein 3B isoform X5 [Homo sapiens]	0.82	0.22	0.19	0.86
PREDICTED: neutrophil cytosol factor 1 isoform X1 [Homo sapiens]	0.82	0.11	0.14	1.24
PREDICTED: neutrophil cytosol factor 1 isoform X2 [Homo sapiens]	0.82	0.11	0.14	1.24
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X7 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X8 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X9 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: voltage-dependent calcium channel subunit alpha-2/delta-1 isoform X10 [Homo sapiens]	1.28	3.53	3.91	1.11
PREDICTED: protein disulfide-isomerase A4 isoform X1 [Homo sapiens]	1.52	1.97	0.85	0.43

PREDICTED: clusterin isoform X1 [Homo sapiens]	0.84	3.71	4.07	1.10
PREDICTED: chondroitin sulfate N- acetylgalactosaminyltransferase 1 isoform X9 [Homo sapiens]	0.66	8.14	6.36	0.81
PREDICTED: testis-expressed sequence 15 protein isoform X4 [Homo sapiens]	1.94	3.76	3.84	1.02
PREDICTED: phosphoprotein associated with glycosphingolipid- enriched microdomains 1 isoform X1 [Homo sapiens]	1.34	0.25	0.15	0.61
PREDICTED: carboxypeptidase Q isoform X2 [Homo sapiens]	2.49	5.70	4.05	0.71
PREDICTED: protein FAM49B isoform X5 [Homo sapiens]	0.89	0.46	0.50	1.10
PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform X1 [Homo sapiens]	1.27	2.06	3.70	1.80
PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform X2 [Homo sapiens]	1.27	2.06	3.70	1.80
PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform X3 [Homo sapiens]	1.27	2.06	3.70	1.80
PREDICTED: ectonucleotide pyrophosphatase/phosphodiesterase family member 2 isoform X4 [Homo sapiens]	1.27	2.06	3.70	1.80
PREDICTED: plectin isoform X10 [Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X11 [Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: plectin isoform X12 [Homo sapiens]	1.37	0.35	0.27	0.76
PREDICTED: probable peptidyl-tRNA hydrolase isoform X1 [Homo sapiens]	0.88	2.30	1.76	0.76
PREDICTED: ficolin-2 isoform X1 [Homo sapiens]	2.24	4.57	4.22	0.92
PREDICTED: gelsolin isoform X7 [Homo sapiens]	1.00	7.20	6.97	0.97
PREDICTED: gelsolin isoform X8 [Homo sapiens]	0.99	6.68	6.72	1.00
PREDICTED: tenascin isoform X5 [Homo sapiens]	0.83	1.23	1.56	1.26

PREDICTED: tenascin isoform X6 [Homo sapiens]	0.82	1.25	1.68	1.35
PREDICTED: tenascin isoform X7 [Homo sapiens]	0.82	1.25	1.68	1.35
PREDICTED: tenascin isoform X8 [Homo sapiens]	0.83	1.23	1.56	1.26
PREDICTED: tenascin isoform X9 [Homo sapiens]	0.84	1.13	1.45	1.29
PREDICTED: tenascin isoform X10 [Homo sapiens]	0.84	1.26	1.45	1.15
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X1 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X3 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X4 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X5 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X6 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X7 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X8 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X9 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X10 [Homo sapiens]	1.28	0.60	0.46	0.77
PREDICTED: thioredoxin isoform X1 [Homo sapiens]	1.43	0.30	0.17	0.58
PREDICTED: vimentin isoform X1 [Homo sapiens]	0.92	0.20	0.11	0.57
PREDICTED: neuropilin-1 isoform X1 [Homo sapiens]	0.95	3.93	3.77	0.96
PREDICTED: neuropilin-1 isoform X2 [Homo sapiens]	0.95	3.93	3.77	0.96

PREDICTED: neuropilin-1 isoform X3 [Homo sapiens]	0.95	3.93	3.77	0.96
PREDICTED: neuropilin-1 isoform X4 [Homo sapiens]	0.95	3.93	3.77	0.96
PREDICTED: neuropilin-1 isoform X5 [Homo sapiens]	0.95	3.93	3.77	0.96
PREDICTED: neuropilin-1 isoform X6 [Homo sapiens]	0.95	3.93	3.77	0.96
PREDICTED: oncoprotein-induced transcript 3 protein isoform X1 [Homo sapiens]	0.95	1.67	1.79	1.07
PREDICTED: mannose-binding protein C isoform X1 [Homo sapiens]	1.27	8.08	5.18	0.64
PREDICTED: mannose-binding protein C isoform X4 [Homo sapiens]	1.19	8.63	5.93	0.69
PREDICTED: multimerin-2 isoform X2 [Homo sapiens]	0.97	9.52	6.89	0.72
PREDICTED: probable E3 ubiquitin- protein ligase TRIM8 isoform X1 [Homo sapiens]	0.76	0.64	0.88	1.16
PREDICTED: probable E3 ubiquitin- protein ligase TRIM8 isoform X2 [Homo sapiens]	0.76	0.64	0.88	1.16
PREDICTED: multiple inositol polyphosphate phosphatase 1 isoform X1 [Homo sapiens]	1.37	19.79	20.69	1.05
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X1 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X2 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X3 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X4 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X5 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B	2.49	43.95	58.97	1.34

member 1 isoform X6 [Homo sapiens]				
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X7 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: amyloid beta A4 precursor protein-binding family B member 1 isoform X8 [Homo sapiens]	2.49	43.95	58.97	1.34
PREDICTED: lymphocyte-specific protein 1 isoform X5 [Homo sapiens]	0.95	0.23	0.24	1.04
PREDICTED: nucleobindin-2 isoform X4 [Homo sapiens]	2.07	0.04	0.46	11.58
PREDICTED: nucleobindin-2 isoform X9 [Homo sapiens]	2.07	0.04	0.46	11.58
PREDICTED: cadherin-related family member 5 isoform X1 [Homo sapiens]	2.07	3.24	4.80	1.48
PREDICTED: receptor-type tyrosine-protein phosphatase eta isoform X1, partial [Homo sapiens]	2.60	4.01	4.25	1.06
PREDICTED: CD44 antigen isoform X11 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X12 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: CD44 antigen isoform X13 [Homo sapiens]	1.28	5.46	4.31	0.79
PREDICTED: interleukin-18-binding protein isoform X7 [Homo sapiens]	1.18	5.96	5.51	0.92
PREDICTED: NADP-dependent malic enzyme, mitochondrial isoform X6 [Homo sapiens]	3.42	4.65	3.61	0.78
PREDICTED: out at first protein homolog isoform X1 [Homo sapiens]	2.60	6.47	5.95	0.92
PREDICTED: cell surface glycoprotein MUC18 isoform X3 [Homo sapiens]	1.90	3.26	3.37	1.03
PREDICTED: cell surface glycoprotein MUC18 isoform X4 [Homo sapiens]	1.90	3.26	3.37	1.03
PREDICTED: cell surface glycoprotein MUC18 isoform X5 [Homo sapiens]	1.90	3.26	3.37	1.03
PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	2.16	0.17	0.14	0.83
PREDICTED: roundabout homolog 4 isoform X4 [Homo sapiens]	0.73	0.46	0.41	0.87
PREDICTED: tyrosine-protein phosphatase non-receptor type 6 isoform X1 [Homo sapiens]	0.64	0.18	0.15	0.82

PREDICTED: alpha-2-macroglobulin isoform X1 [Homo sapiens]	0.56	2.07	1.76	0.85
PREDICTED: L-lactate dehydrogenase B chain isoform X1 [Homo sapiens]	0.88	0.36	0.37	1.03
PREDICTED: complement C1r subcomponent-like protein isoform X4 [Homo sapiens]	1.19	9.59	10.57	1.10
PREDICTED: complement C1r subcomponent-like protein isoform X5 [Homo sapiens]	1.19	9.59	10.57	1.10
PREDICTED: keratin, type II cytoskeletal 3 isoform X2 [Homo sapiens]	0.68	0.11	0.11	0.94
PREDICTED: keratin, type II cytoskeletal 3 isoform X3 [Homo sapiens]	0.68	0.11	0.11	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase beta isoform X3 [Homo sapiens]	0.88	1.12	1.18	1.06
PREDICTED: receptor-type tyrosine-protein phosphatase beta isoform X4 [Homo sapiens]	0.88	1.12	1.18	1.06
PREDICTED: receptor-type tyrosine-protein phosphatase beta isoform X5 [Homo sapiens]	0.88	1.12	1.18	1.06
PREDICTED: von Willebrand factor A domain-containing protein 8 isoform X1 [Homo sapiens]	1.79	26.69	17.45	0.65
PREDICTED: von Willebrand factor A domain-containing protein 8 isoform X2 [Homo sapiens]	1.79	26.69	17.45	0.65
PREDICTED: von Willebrand factor A domain-containing protein 8 isoform X3 [Homo sapiens]	1.79	26.69	17.45	0.65
PREDICTED: coagulation factor VII isoform X1 [Homo sapiens]	0.88	4.76	4.39	0.92
PREDICTED: coagulation factor X isoform X2 [Homo sapiens]	1.43	6.22	5.71	0.92
PREDICTED: epididymal secretory protein E1 isoform X1 [Homo sapiens]	0.60	3.33	2.67	0.82
PREDICTED: serpin A11 isoform X1 [Homo sapiens]	1.74	4.72	4.88	1.03
PREDICTED: proteasome activator complex subunit 2 isoform X1 [Homo sapiens]	1.40	0.44	0.33	0.74
PREDICTED: proteasome activator complex subunit 2 isoform X2 [Homo sapiens]	1.40	0.44	0.33	0.74

sapiens]				
PREDICTED: calmodulin isoform X1 [Homo sapiens]	1.52	0.08	0.05	0.68
PREDICTED: dmX-like protein 2 isoform X8 [Homo sapiens]	0.93	9.72	12.08	1.24
PREDICTED: SHC-transforming protein 4 isoform X3 [Homo sapiens]	1.43	20.57	13.57	0.66
PREDICTED: pyruvate kinase PKM isoform X4 [Homo sapiens]	0.99	0.20	0.18	0.92
PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member A isoform X1 [Homo sapiens]	0.88	0.23	0.23	1.03
PREDICTED: talin-2 isoform X12 [Homo sapiens]	1.90	0.68	0.88	1.30
PREDICTED: talin-2 isoform X13 [Homo sapiens]	1.90	0.68	0.88	1.30
PREDICTED: talin-2 isoform X14 [Homo sapiens]	1.90	0.68	0.88	1.30
PREDICTED: talin-2 isoform X15 [Homo sapiens]	1.90	0.68	0.88	1.30
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X1 [Homo sapiens]	0.88	0.04	0.93	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X2 [Homo sapiens]	0.88	0.04	0.93	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X3 [Homo sapiens]	0.88	0.04	0.93	24.95
PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X4 [Homo sapiens]	0.88	0.04	0.93	24.95
PREDICTED: integrin alpha-M isoform X1 [Homo sapiens]	1.00	0.32	0.28	0.89
PREDICTED: myc-associated zinc finger protein isoform X1 [Homo sapiens]	0.83	1.90	1.98	1.04
PREDICTED: myc-associated zinc finger protein isoform X2 [Homo sapiens]	0.83	1.90	1.98	1.04
PREDICTED: cadherin-13 isoform X1 [Homo sapiens]	1.28	1.50	1.47	0.98
PREDICTED: cholesteryl ester transfer protein isoform X1 [Homo sapiens]	1.27	7.24	3.32	0.46
PREDICTED: haptoglobin-related protein isoform X1 [Homo sapiens]	0.73	0.41	0.49	1.59

PREDICTED: asialoglycoprotein receptor 2 isoform X5 [Homo sapiens]	0.83	4.65	4.50	0.97
PREDICTED: asialoglycoprotein receptor 2 isoform X6 [Homo sapiens]	0.83	4.65	4.50	0.97
PREDICTED: asialoglycoprotein receptor 2 isoform X7 [Homo sapiens]	0.83	4.65	4.50	0.97
PREDICTED: sex hormone-binding globulin isoform X7 [Homo sapiens]	2.60	3.99	6.21	1.56
PREDICTED: collagen alpha-1(I) chain isoform X1 [Homo sapiens]	0.45	0.23	0.21	0.90
PREDICTED: collagen alpha-1(I) chain isoform X2 [Homo sapiens]	0.45	0.23	0.21	0.90
PREDICTED: collagen alpha-1(I) chain isoform X3 [Homo sapiens]	0.30	0.21	0.22	0.98
PREDICTED: angiotensin-converting enzyme isoform X2 [Homo sapiens]	1.28	5.38	4.78	0.89
PREDICTED: alpha-N-acetylglucosaminidase isoform X1 [Homo sapiens]	6.90	2.32	1.20	0.52
PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens]	0.88	0.17	0.17	1.03
PREDICTED: actin, cytoplasmic 2 isoform X2 [Homo sapiens]	2.60	0.14	0.08	0.61
PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X1 [Homo sapiens]	0.95	0.62	0.74	1.18
PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X2 [Homo sapiens]	0.95	0.62	0.74	1.18
PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X3 [Homo sapiens]	0.95	0.62	0.74	1.18
PREDICTED: receptor-type tyrosine-protein phosphatase mu isoform X4 [Homo sapiens]	0.95	0.62	0.74	1.18
PREDICTED: serpin B8 isoform X1 [Homo sapiens]	2.66	0.37	0.35	0.95
PREDICTED: N-acetylmuramoyl-L-alanine amidase isoform X1 [Homo sapiens]	0.95	6.04	5.62	0.93
PREDICTED: glucosidase 2 subunit beta isoform X1 [Homo sapiens]	1.52	0.80	0.76	0.95
PREDICTED: glucosidase 2 subunit beta isoform X3 [Homo sapiens]	1.52	0.80	0.76	0.95
PREDICTED: glucosidase 2 subunit	1.52	0.80	0.76	0.95

beta isoform X4 [Homo sapiens]				
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X14 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X15 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X16 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X17 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X18 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X19 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X20 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X21 [Homo sapiens]	0.65	1.24	1.23	0.94
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X22 [Homo sapiens]	0.65	3.27	2.71	0.83
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X23 [Homo sapiens]	0.65	3.27	2.71	0.83
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X24 [Homo sapiens]	0.65	3.27	2.71	0.83
PREDICTED: receptor-type tyrosine-protein phosphatase S isoform X25 [Homo sapiens]	0.65	3.27	2.71	0.83
PREDICTED: scaffold attachment factor B1 isoform X1 [Homo sapiens]	1.41	0.78	0.49	0.63
PREDICTED: syntaxin-binding protein 2 isoform X1 [Homo sapiens]	1.26	0.06	0.05	0.83
PREDICTED: tropomyosin alpha-4 chain isoform X2 [Homo sapiens]	1.90	0.60	0.54	0.90
PREDICTED: sialic acid-binding Ig-like lectin 14 isoform X1 [Homo sapiens]	0.93	2.97	2.45	0.83
PREDICTED: UPF0692 protein				
C19orf54 isoform X4 [Homo sapiens]	0.17	0.19	0.14	0.80
PREDICTED: spectrin beta chain, non-	0.88	0.28	0.21	0.75

erythrocytic 4 isoform X1 [Homo sapiens]				
PREDICTED: alpha-actinin-4 isoform X3 [Homo sapiens]	0.88	0.28	0.21	0.76
PREDICTED: endothelial protein C receptor isoform X2 [Homo sapiens]	0.99	9.42	6.92	0.73
PREDICTED: endothelial protein C receptor isoform X1 [Homo sapiens]	0.99	9.42	6.92	0.73
PREDICTED: ICOS ligand-like isoform X1 [Homo sapiens]	0.84	3.62	5.08	1.40
PREDICTED: ICOS ligand-like isoform X2 [Homo sapiens]	0.84	3.62	5.08	1.40
PREDICTED: histone H2B type F-S-like [Homo sapiens]	3.29	0.22	0.07	0.32
PREDICTED: collagen alpha-1(VI) chain isoform X1 [Homo sapiens]	0.88	1.55	1.37	0.88
PREDICTED: integrin beta-2 isoform X1 [Homo sapiens]	0.89	0.37	0.32	0.86
PREDICTED: neurofilament heavy polypeptide isoform X2 [Homo sapiens]	1.00	0.35	0.44	1.26
PREDICTED: ras-related C3 botulinum toxin substrate 2 isoform X1 [Homo sapiens]	0.84	0.22	0.16	0.72
PREDICTED: DEP domain-containing protein 5 isoform X9 [Homo sapiens]	1.43	0.77	1.44	1.88
PREDICTED: DEP domain-containing protein 5 isoform X10 [Homo sapiens]	1.43	0.77	1.44	1.88
PREDICTED: thyroxine-binding globulin isoform X2 [Homo sapiens]	0.77	4.64	3.07	0.72
PREDICTED: coagulation factor IX isoform X3 [Homo sapiens]	1.28	8.31	8.96	1.08
PREDICTED: mastermind-like domain-containing protein 1 isoform X5 [Homo sapiens]	0.78	0.36	0.35	0.92
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	0.84	0.08	0.21	2.58
PREDICTED: HLA class I histocompatibility antigen, alpha chain G isoform X1 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: cadherin-related family member 5 isoform X1 [Homo sapiens]	2.07	3.24	4.80	1.48
PREDICTED: cadherin-related family member 5 isoform X2 [Homo sapiens]	2.07	3.24	4.80	1.48

sapiens]				
PREDICTED: cadherin-related family member 5 isoform X3 [Homo sapiens]	2.07	3.24	4.80	1.48
PREDICTED: cadherin-related family member 5 isoform X4 [Homo sapiens]	2.07	3.24	4.80	1.48
PREDICTED: protein Z-dependent protease inhibitor isoform X1 [Homo sapiens]	2.79	13.47	9.72	0.72
PREDICTED: liver carboxylesterase 1-like [Homo sapiens]	1.69	6.12	1.35	0.22
PREDICTED: alpha-2-antiplasmin isoform X1 [Homo sapiens]	2.24	6.75	6.21	0.92
PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	0.99	0.13	0.12	0.99
PREDICTED: D-dopachrome decarboxylase isoform X1 [Homo sapiens]	0.99	0.22	0.10	0.46
PREDICTED: V-set and immunoglobulin domain-containing protein 1-like [Homo sapiens]	0.76	0.23	0.69	1.96
PREDICTED: apolipoprotein M isoform X1 [Homo sapiens]	0.76	2.49	1.31	0.61
PREDICTED: HLA class I histocompatibility antigen, B-15 alpha chain isoform X2 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, B-15 alpha chain isoform X3 [Homo sapiens]	0.73	1.81	1.60	0.87
PREDICTED: HLA class I histocompatibility antigen, alpha chain G isoform X1 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X3 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X4 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X5 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: HLA class I histocompatibility antigen, alpha chain F isoform X6 [Homo sapiens]	0.81	2.02	2.41	1.63
PREDICTED: protein CutA isoform X1	0.70	0.13	0.18	1.16

[Homo sapiens]				
PREDICTED: macrophage mannose receptor 1 [Homo sapiens]	1.00	2.51	2.50	1.00
PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-like [Homo sapiens]	0.78	0.75	1.92	1.76
PREDICTED: uncharacterized protein LOC102725101 [Homo sapiens]	1.26	10.11	2.80	0.28
PREDICTED: histone H2B type F-S-like [Homo sapiens]	3.29	0.22	0.07	0.32
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X1 [Homo sapiens]	0.62	0.91	0.68	0.78
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X2 [Homo sapiens]	0.62	0.91	0.68	0.78
PREDICTED: leukocyte immunoglobulin-like receptor subfamily A member 3-like isoform X3 [Homo sapiens]	0.62	0.91	0.68	0.78
putative alpha-1-antitrypsin-related protein precursor [Homo sapiens]	1.43	18.21	13.51	0.74
bridging integrator 2 isoform 4 [Homo sapiens]	1.24	4.69	3.70	0.79
bridging integrator 2 isoform 1 [Homo sapiens]	1.24	4.69	3.70	0.79
bridging integrator 2 isoform 3 [Homo sapiens]	1.24	4.69	3.70	0.79
bridging integrator 2 isoform 2 [Homo sapiens]	1.24	4.69	3.70	0.79
ribosyldihydronicotinamide dehydrogenase [quinone] isoform 2 [Homo sapiens]	0.76	0.48	0.40	0.84
dedicator of cytokinesis protein 10 DOCK10.2 [Homo sapiens]	1.74	41.25	57.82	1.40
T-cell acute lymphocytic leukemia protein 1 isoform 2 [Homo sapiens]	1.00	5.58	8.85	1.59
voltage-dependent calcium channel subunit alpha-2/delta-2 isoform d [Homo sapiens]	2.49	11.30	11.75	1.04
polyubiquitin-C [Homo sapiens]	1.74	0.34	0.39	1.15
peptidyl-prolyl cis-trans isomerase A-like 4A/B/C [Homo sapiens]	1.74	0.17	0.12	0.74
poliovirus receptor isoform alpha precursor [Homo sapiens]	1.18	7.34	8.79	1.20

poliovirus receptor isoform delta precursor [Homo sapiens]	1.18	7.34	8.79	1.20
seprase isoform 2 [Homo sapiens]	1.40	15.36	15.15	0.99
basement membrane-specific heparan sulfate proteoglycan core protein isoform a precursor [Homo sapiens]	0.95	2.98	3.19	1.07
polypeptide N-acetylglucosaminyltransferase 2 isoform 2 [Homo sapiens]	1.74	2.59	2.76	1.06
ras-related protein Rap-1A precursor [Homo sapiens]	0.95	0.11	0.08	0.72
SPARC-like protein 1 isoform 2 [Homo sapiens]	2.79	10.04	12.10	1.21
carbonic anhydrase 1 isoform b [Homo sapiens]	0.84	0.19	0.14	0.77
carbonic anhydrase 1 isoform c [Homo sapiens]	0.84	0.19	0.14	0.73
carboxypeptidase N subunit 2 precursor [Homo sapiens]	0.95	4.62	5.89	1.27
beta-hexosaminidase subunit beta isoform 2 [Homo sapiens]	1.43	0.68	0.64	0.95
tubulin beta chain isoform a [Homo sapiens]	0.83	0.12	0.11	0.92
tubulin beta chain isoform c [Homo sapiens]	1.27	0.26	0.28	1.10
tubulin beta chain isoform d [Homo sapiens]	0.83	0.12	0.11	0.92
tubulin beta chain isoform e [Homo sapiens]	0.83	0.12	0.11	0.92
carbonic anhydrase 2 isoform 2 [Homo sapiens]	0.78	0.17	0.11	0.69
hepatocyte growth factor activator isoform 1 preproprotein [Homo sapiens]	0.95	3.53	2.80	0.79
(Bos taurus) 81 kDa protein	5.64	12.68	7.01	0.55
(Bos taurus) similar to Complement C4-A precursor	0.92	4.10	3.18	0.78
(Bos taurus) hypothetical protein	1.34	11.30	9.94	0.88
(Bos taurus) similar to fibulin-1 C isoform 1	0.88	2.14	1.83	0.86
(Bos taurus) similar to peptidoglycan recognition protein L	0.88	6.58	4.50	0.68
(Bos taurus) 54 kDa protein	1.58	6.67	6.98	1.05
(Bos taurus) 55 kDa protein	1.47	16.14	10.96	0.68
(Bos taurus) 68 kDa protein	1.28	3.79	3.18	0.84
(Bos taurus) 121 kDa protein	1.28	8.22	8.96	1.09

(Bos taurus) similar to apolipoprotein B, partial	0.99	3.57	4.57	1.28
(Bos taurus) 63 kDa protein	0.18	0.56	0.63	1.17
SWISS-PROT:O95678 Tax_Id=9606				
Gene_Symbol=KRT75 Keratin, type II cytoskeletal 75	0.73	0.17	0.12	0.76
SWISS-PROT:P00735 (Bos taurus)				
Prothrombin precursor (Fragment)	1.74	5.58	3.47	0.62
Trypsin - Sus scrofa (Pig).	0.93	1.27	1.19	0.94
SWISS-PROT:P01030 (Bos taurus)				
similar to Complement C4-A precursor	0.92	4.10	3.18	0.78
SWISS-PROT:P01966 (Bos taurus)				
Hemoglobin subunit alpha	0.56	0.50	0.32	0.71
SWISS-PROT:P02070 (Bos taurus)				
Hemoglobin subunit beta	0.55	0.17	0.12	0.75
SWISS-PROT:P02533 Tax_Id=9606				
Gene_Symbol=KRT14 Keratin, type I cytoskeletal 14	0.45	0.11	0.07	0.74
SWISS-PROT:P02535-1 Tax_Id=10090				
Gene_Symbol=Krt10 Isoform 1 of Keratin, type I cytoskeletal 10	0.27	0.26	0.37	1.20
SWISS-PROT:P02538 Tax_Id=9606				
Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A	0.73	0.14	0.11	0.84
SWISS-PROT:P02584 (Bos taurus)				
Profilin-1	0.83	0.14	0.07	0.50
SWISS-PROT:P02672 (Bos taurus)				
Fibrinogen alpha chain precursor	1.79	0.08	0.05	0.62
SWISS-PROT:P02676 (Bos taurus)				
similar to Fibrinogen beta chain precursor	1.69	0.13	0.12	0.97
SWISS-PROT:P02768-1 Tax_Id=9606				
Gene_Symbol=ALB Isoform 1 of Serum albumin precursor	0.67	0.08	0.81	4.45
SWISS-PROT:P02769 (Bos taurus)				
Bovine serum albumin precursor	1.35	0.08	0.05	0.65
SWISS-PROT:P04258 (Bos taurus)				
Similar to Collagen alpha 1(III) chain	0.60	0.82	0.75	0.89
SWISS-PROT:P04259 Tax_Id=9606				
Gene_Symbol=KRT6B Keratin, type II cytoskeletal 6B	0.73	0.14	0.11	0.84
SWISS-PROT:P04264 Tax_Id=9606				
Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1	0.24	0.30	0.27	0.88
SWISS-PROT:P06868 (Bos taurus)				
Plasminogen precursor	0.97	4.12	4.52	1.10
SWISS-PROT:P07224 (Bos taurus)	1.90	4.52	4.91	1.09

Vitamin K-dependent protein S precursor				
SWISS-PROT:P07477 Tax_Id=9606				
Gene_Symbol=PRSS1 Trypsin-1 precursor	0.95	0.78	0.75	0.97
SWISS-PROT:P08729 Tax_Id=9606				
Gene_Symbol=KRT7 Keratin, type II cytoskeletal 7	0.79	0.14	0.15	1.25
SWISS-PROT:P12035 Tax_Id=9606				
Gene_Symbol=KRT3 Keratin, type II cytoskeletal 3	0.68	0.11	0.11	0.94
SWISS-PROT:P12763 (Bos taurus)				
Alpha-2-HS-glycoprotein precursor	1.90	6.96	7.37	1.06
SWISS-PROT:P13645 Tax_Id=9606				
Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10	0.40	0.29	0.41	1.28
SWISS-PROT:P13647 Tax_Id=9606				
Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5	0.73	0.24	0.27	1.12
SWISS-PROT:P15497 (Bos taurus)				
Apolipoprotein A-I precursor	0.57	0.14	0.05	0.46
SWISS-PROT:P17690 (Bos taurus)				
Beta-2-glycoprotein 1 precursor	2.07	7.83	4.55	0.58
SWISS-PROT:P21752 (Bos taurus)				
Thymosin beta-9	0.71	0.91	0.65	0.75
SWISS-PROT:P28800 (Bos taurus)				
Alpha-2-antiplasmin precursor	2.24	6.91	6.60	0.96
SWISS-PROT:P31096 Osteopontin - Bos taurus (Bovine).	1.43	2.15	2.00	0.93
SWISS-PROT:P34955 (Bos taurus)				
Alpha-1-antiproteinase precursor	1.90	0.92	0.44	0.48
SWISS-PROT:P35527 Tax_Id=9606				
Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9	0.55	1.09	0.70	0.71
SWISS-PROT:P35908 Tax_Id=9606				
Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal	0.34	0.21	0.30	1.18
SWISS-PROT:P41361 (Bos taurus)				
Antithrombin-III precursor	1.27	2.13	1.93	0.91
SWISS-PROT:P50446 Tax_Id=10090				
Gene_Symbol=Krt6a Keratin, type II cytoskeletal 6A	0.68	0.30	0.39	1.11
SWISS-PROT:Q03247 (Bos taurus)				
Apolipoprotein E precursor	0.96	7.21	7.60	1.05
SWISS-PROT:Q05443 (Bos taurus)				
Lumican precursor	0.93	11.11	9.30	0.84
TREMBL:Q0IIK2 (Bos taurus)				
Transferrin	0.91	0.09	0.15	1.70

TREMBL:Q0V8M9;Q9TRI0 (Bos taurus) similar to inter-alpha (globulin) inhibitor H3 isoform 2	0.84	0.50	0.88	1.76
TREMBL:Q0VCM5 (Bos taurus) Similar to Inter-alpha-trypsin inhibitor heavy chain H1	2.79	11.00	12.79	1.16
SWISS-PROT:Q14CN4-1 Tax_Id=9606 Gene_Symbol=KRT72 Isoform 1 of Keratin, type II cytoskeletal 72	0.73	0.17	0.12	0.76
TREMBL:Q1A7A4 (Bos taurus) similar to complement component C5	2.24	6.15	7.07	1.15
SWISS-PROT:Q28065 (Bos taurus) C4b-binding protein alpha chain precursor	0.79	3.38	4.47	1.14
SWISS-PROT:Q28107 (Bos taurus) Coagulation factor V precursor	0.99	5.42	5.51	1.02
TREMBL:Q28194 (Bos taurus) Thrombospondin-1	1.74	5.41	5.61	1.04
SWISS-PROT:Q29443 Serotransferrin - Bos taurus (Bovine).	0.91	0.09	0.15	1.70
SWISS-PROT:Q29RQ1 (Bos taurus) Complement component C7 precursor	0.95	5.95	5.97	1.00
TREMBL:Q2HJF0 (Bos taurus) Similar to Serotransferrin	0.64	0.13	0.11	0.84
TREMBL:Q2KIG3 (Bos taurus) Similar to carboxypeptidase B2	0.84	12.46	14.24	1.14
SWISS-PROT:Q2KIS7 (Bos taurus) Tetranectin precursor	0.95	4.26	3.18	0.75
TREMBL:Q2KJ83 (Bos taurus) Similar to Carboxypeptidase N catalytic chain	0.99	5.11	6.45	1.26
TREMBL:Q2KJC7;Q8HZM3 (Bos taurus) Periostin, osteoblast specific factor	2.49	0.73	0.82	1.11
TREMBL:Q2KJF1 (Bos taurus) Alpha-1-B glycoprotein	1.21	11.60	12.90	1.11
SWISS-PROT:Q2UVX4 (Bos taurus) Complement C3 precursor	0.77	0.13	0.07	0.62
TREMBL:Q32PI4 (Bos taurus) Similar to complement factor I	1.28	11.48	13.50	1.18
SWISS-PROT:Q32PJ2 (Bos taurus) Apolipoprotein A-IV precursor	2.49	10.04	10.36	1.03
TREMBL:Q3KNV1;Q96GE1 Tax_Id=9606 Gene_Symbol=KRT7 keratin 7	0.79	0.14	0.15	1.25
TREMBL:Q3KUS7 (Bos taurus) Complement factor B	0.76	3.47	2.73	0.86

TREMBL:Q3MHH8 (Bos taurus) Amylase, alpha 2B; pancreatic	0.96	1.49	2.41	1.62
SWISS-PROT:Q3MHN2 (Bos taurus) Complement component C9 precursor	2.24	5.30	6.76	1.28
SWISS-PROT:Q3MHN5 (Bos taurus) Vitamin D-binding protein precursor	1.58	6.67	6.98	1.05
TREMBL:Q3SX09 (Bos taurus) similar to HBG protein	0.63	0.35	0.39	1.20
TREMBL:Q3SX14 (Bos taurus) Similar to Gelsolin	0.79	2.40	2.57	0.99
TREMBL:Q3SX28;Q5KR48 (Bos taurus) Tropomyosin 2	2.79	0.77	0.63	0.82
TREMBL:Q3T052;Q5EA67 (Bos taurus) Inter-alpha (Globulin) inhibitor H4	1.54	2.49	1.25	0.50
SWISS-PROT:Q3TTY5 Tax_Id=10090 Gene_Symbol=Krt2 Keratin, type II cytoskeletal 2 epidermal	0.19	0.44	0.57	1.11
SWISS-PROT:Q3Y5Z3 (Bos taurus) Adiponectin precursor	1.28	3.96	10.84	2.74
TREMBL:Q3ZAW8;Q9EQD6;Q9EQD7 Tax_Id=10090 Gene_Symbol=Krt16 Keratin intermediate filament 16a	0.45	0.11	0.07	0.74
SWISS-PROT:Q3ZBD7 (Bos taurus) Glucose-6-phosphate isomerase	2.16	0.18	0.18	1.02
TREMBL:Q3ZBS7 (Bos taurus) Vitronectin	1.90	7.34	4.18	0.57
SWISS-PROT:Q5XKE5 Tax_Id=9606 Gene_Symbol=KRT79 Keratin, type II cytoskeletal 79	0.73	0.35	0.69	1.49
SWISS-PROT:Q5XQN5 (Bos taurus) Keratin, type II cytoskeletal 5	0.48	0.35	0.45	1.13
TREMBL:Q6IME9 Tax_Id=10090 Gene_Symbol=Krt72 Type-II keratin Kb35	0.73	0.17	0.12	0.76
TREMBL:Q6ISB0 Keratin, hair, basic, 4 - Homo sapiens (Human).	0.79	0.14	0.15	1.25
TREMBL:Q6T181;Q6T182 (Bos taurus) similar to sex hormone- binding globulin	1.28	8.69	14.61	1.68
TREMBL:Q8BGZ7;Q99MH7 Tax_Id=10090 Gene_Symbol=Krt75 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732475I03	0.11	0.36	0.45	1.95
product:CYTOKERATIN homolog SWISS-PROT:Q922U2 Tax_Id=10090	0.48	0.35	0.45	1.13

Gene_Symbol=Krt5 Keratin, type II cytoskeletal 5 SWISS-PROT:Q95121 (Bos taurus) Pigment epithelium-derived factor precursor	2.07	10.77	10.04	0.93
SWISS-PROT:Q9DCV7 Tax_Id=10090 Gene_Symbol=Krt7 Keratin, type II cytoskeletal 7 TREMBL:Q9H552 Tax_Id=9606	0.79	0.14	0.15	1.25
Gene_Symbol=- Keratin-8-like protein 1 SWISS-PROT:Q9NSB2 Keratin, type II cuticular Hb4 (Hair keratin, type II Hb4) - Homo sapiens (Human). TREMBL:Q9TRI1 (Bos taurus) similar to inter-alpha-trypsin inhibitor heavy chain2	0.79	0.14	0.15	1.25
SWISS-PROT:Q9Z2K1 Tax_Id=10090 Gene_Symbol=Krt16 Keratin, type I cytoskeletal 16 (Bos taurus) similar to afamin	1.44	24.71	24.76	1.00
	0.45	0.11	0.07	0.74
	0.81	6.26	6.17	0.93